

TITLE OF

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protein - protein search, using sw model

January 14, 2003, 18:39:18 : Search time 14 Seconds
(without alignments)
39.931 Million cell updates/sec

Run on:

US-09-828-645-1

Title: 119
Perfect score: 1 DICTMHYTNMTHYICEE 19

Sequence:

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : Issued Patents, AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/backfilest.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	20	US-08-934-915-28	Sequence 28, Appl
2	119	100.0	365	US-08-472-666-4	Sequence 4, Appl
3	119	100.0	365	US-09-362-012A-2	Sequence 2, Appl
4	119	100.0	365	US-09-362-012A-5	Sequence 5, Appl
5	119	100.0	365	US-08-934-915-178	Sequence 178, Appl
6	119	100.0	20	US-08-934-915-31	Sequence 31, Appl
7	109	95.8	20	US-08-934-915-136	Sequence 136, Appl
8	104	87.4	20	US-08-934-915-177	Sequence 177, Appl
9	96	80.7	20	US-08-934-915-69	Sequence 69, Appl
10	79	66.4	20	US-08-934-915-74	Sequence 74, Appl
11	52	43.7	20	US-08-934-915-13	Sequence 13, Appl
12	52	43.7	20	US-08-934-915-7	Sequence 7, Appl
13	47	39.5	20	US-09-000-094-46	Sequence 46, Appl
14	47	39.5	1587	US-09-000-094-46	Sequence 2, Appl
15	44	37.0	19	US-08-685-922-6	Sequence 6, Appl
16	43	36.1	257	US-09-144-925-6	Sequence 32, Appl
17	43	35.3	20	US-08-934-915-32	Sequence 2992, Appl
18	42	35.3	154	US-09-134-001C-2992	Sequence 15, Appl
19	42	35.3	251	US-08-685-922-15	Sequence 15, Appl
20	42	35.3	251	US-09-144-925-15	Sequence 2920, Appl
21	42	35.3	251	US-09-134-001C-2920	Sequence 19, Appl
22	42	35.3	489	US-09-134-001C-2920	Sequence 19, Appl
23	42	35.3	500	US-08-705-771-19	Sequence 4, Appl
24	41	34.5	265	US-08-807-044-1	Sequence 4, Appl
25	41	34.5	600	US-08-370-156-4	Sequence 4, Appl
26	41	34.5	600	US-08-814-095-4	Sequence 4, Appl
27	41	34.5	600	US-08-814-095-4	Sequence 4, Appl

28	41	34.5	600	4	US-08-975-084-1	Sequence 1, Appl
29	41	34.5	614	1	US-07-732-962A-2	Sequence 2, Appl
30	41	34.5	614	2	US-08-370-156-2	Sequence 19, Appl
31	41	34.5	614	3	US-08-446-100-19	Sequence 20, Appl
32	41	34.5	614	3	US-08-446-100-20	Sequence 21, Appl
33	41	34.5	614	3	US-08-446-100-21	Sequence 22, Appl
34	41	34.5	614	3	US-08-446-100-22	Sequence 23, Appl
35	41	34.5	614	3	US-08-446-100-23	Sequence 24, Appl
36	41	34.5	614	3	US-08-446-100-25	Sequence 25, Appl
37	41	34.5	614	3	US-08-814-095-2	Sequence 2, Appl
38	41	34.5	614	5	PCT-US92-06106-2	Sequence 6, Appl
39	41	34.5	617	2	US-08-370-156-6	Sequence 80, Appl
40	41	34.5	617	3	US-08-814-095-6	Sequence 60, Appl
41	40	33.6	238	4	US-09-257-179-80	Sequence 60, Appl
42	40	33.6	238	4	US-08-118-270-60	Sequence 60, Appl
43	40	33.6	233	5	PCT-US93-08528-60	Sequence 62, Appl
44	40	33.6	313	3	US-08-926-842B-62	Sequence 62, Appl
45	40	33.6	333	3	US-08-988-876-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-934-915-28
Sequence 28, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17157 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION/DOCKET NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-28
Query Match 100.0%, Score 119, DB 2, Length 20:
Best Local Similarity 100.0%, Pred. No. 3e-11:

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D1CNTMYTNTWTHYICEE 19
Db 2 D1CNTMYTNTWTHYICEE 20

RESULT 2

US-08-472-666-4
; Sequence 4, Application US/08472666
; Patent No. 5821048
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John D.
; APPLICANT: Yasugi, Toshiharu
; TITLE OF INVENTION: METHOD AND KIT FOR DIAGNOSING
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ann-Louise Kerner, Ph.D.
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 01209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,666
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, Patricia A.
; REGISTRATION NUMBER: 33,194
; TELEPHONE: 617-330-1311
; TELECOMMUNICATION INFORMATION: HAZ-010
; INFORMATION FOR SEQ ID NO: 1
; TELEFAX: 617-330-1311
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Papillomavirus-16 E2
; STRAIN: HPV-16 E2
US-08-472-666-4

Query Match
Best Local Similarity 100.0%; Score 119; DB 2; Length 365;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D1CNTMYTNTWTHYICEE 19
Db 124 D1CNTMYTNTWTHYICEE 142

RESULT 3
US-09-362-012A-2
; Sequence 2, Application US/09362012A
; Patent No. 6432926
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Downanick-Morrisette, Jennifer J.
; APPLICANT: Benson, John D.
; APPLICANT: Sakai, Hiroyuki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,012A
FILING DATE: 27-Jul-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/677,206
FILING DATE: 09 JUL 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-362-012A-2

Query Match
Best Local Similarity 100.0%; Score 119; DB 4; Length 365;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D1CNTMYTNTWTHYICEE 19
Db 124 D1CNTMYTNTWTHYICEE 142

RESULT 4
US-09-362-012A-5
; Sequence 5, Application US/09362012A
; Patent No. 6432926
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Downanick-Morrisette, Jennifer J.
; APPLICANT: Benson, John D.
; APPLICANT: Sakai, Hiroyuki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,012A
; FILING DATE: 27-Jul-1999

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/677,206
FILING DATE: 09 JUL 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: HMI-017CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-362-012A-5

Query Match 100.0%; Score 119; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 7e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 D1CNTMHTMTWTHIYCEE 19
DB 124 D1CNTMHTMTWTHIYCEE 142

RESULT 5
PCT-US96-07615-4
Sequence 4, Application PC/TUS9607615
GENERAL INFORMATION:
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: METHODS, KITS, AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: PAPILLOMAVIRUS INFECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmet
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 01209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07615
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HAZ-010PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human papillomavirus-16 E2
STRAIN: HPV-16 E2
PCT-US96-07615-4

Query Match 100.0%; Score 119; DB 5; Length 365;
Best Local Similarity 100.0%; Pred. No. 7e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 D1CNTMHTMTWTHIYCEE 19
DB 124 D1CNTMHTMTWTHIYCEE 142

RESULT 6
US-08-934-915-178
Sequence 178, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-178

Query Match 95.8%; Score 114; DB 2; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.6e-10;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 D1CNTMHTMTWTHIYCEE 19
DB 2 D1CNTMHTMTWTHIYCEE 20

RESULT 7
US-08-934-915-31
Sequence 31, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-31

Query Match 91.68; Score 109; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTMHTMTHTIYC 17
Db 4 DICTMHTMTHTIYC 20

RESULT 8
US-08-934-915-136
Sequence 136, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-136

Query Match 87.4%; Score 104; DB 2; Length 20;
Best Local Similarity 94.1%; Pred. No. 4.5e-09;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTMHTMTHTIYC 17
Db 4 NICMHTMTHTIYC 20

RESULT 9
US-08-934-915-177
Sequence 177, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 177:

SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-934-915-177

Query Match 80.7%; Score 96; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.5e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DICTMHTNTMTHIY 15
 Db 6 DICTMHTMTHIY 20

RESULT 10
 US-08-934-915-69
 ; Sequence 69, Application US/08934915
 ; Patent No. 5932412
 ; GENERAL INFORMATION:
 ; APPLICANT: DILLNER, JOAKIM
 ; APPLICANT: DILLNER, LENA
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 ; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
 ; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
 ; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
 ; NUMBER OF SEQUENCES: 193
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: MASON & ASSOCIATES, P.A.
 ; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 ; CITY: CLEARWATER
 ; STATE: FLORIDA
 ; COUNTRY: U.S.A.
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 3.0
 ; SOFTWARE: Microsoft word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,915
 ; FILING DATE: 22-SEP-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/949,836
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LOUISE A. FOUTCH
 ; REGISTRATION NUMBER: 37,133
 ; REFERENCE/DOCKET NUMBER: 1946.6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 813-538-3800
 ; TELEFAX: 813-538-3820
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 69:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-934-915-69

Query Match 66.4%; Score 79; DB 2; Length 20;
 Best Local Similarity 70.6%; Pred. No. 1.9e-05;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 DICTMHTNTMTHIY 17
 Db 4 DVHNTMHTNMKFTYLC 20

RESULT 11
 US-08-934-915-74
 ; Sequence 74, Application US/08934915
 ; Patent No. 5932412
 ; GENERAL INFORMATION:
 ; APPLICANT: DILLNER, JOAKIM
 ; APPLICANT: DILLNER, LENA
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 ; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
 ; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
 ; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
 ; NUMBER OF SEQUENCES: 193
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: MASON & ASSOCIATES, P.A.
 ; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 ; CITY: CLEARWATER
 ; STATE: FLORIDA
 ; COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 3.0
 SOFTWARE: Microsoft word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,915
 FILING DATE: 22-SEP-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/949,836
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: LOUISE A. FOUTCH
 REGISTRATION NUMBER: 37,133
 REFERENCE/DOCKET NUMBER: 1946.6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 813-538-3800
 TELEFAX: 813-538-3820
 TELEX:
 INFORMATION FOR SEQ ID NO: 74:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-934-915-74

Query Match 47.9%; Score 57; DB 2; Length 20;
 Best Local Similarity 76.9%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 4 NTMDYTNMGEIYI 16
 Db 7 NTMDYTNMGEIYI 19

RESULT 12
 US-08-934-915-13
 ; Sequence 13, Application US/08934915
 ; Patent No. 5932412
 ; GENERAL INFORMATION:
 ; APPLICANT: DILLNER, JOAKIM
 ; APPLICANT: DILLNER, LENA
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 ; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
 ; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
 ; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
 ; NUMBER OF SEQUENCES: 193
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: MASON & ASSOCIATES, P.A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-13

Query Match 43.7%; Score 52; DB 2; Length 20;
Best Local Similarity 61.5%; Pred. No. 0.16;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 4 NTMHYTNMTHIYI 16
| | | | | | | | | |
DB 7 NMEDYVWTHIYL 19

RESULT 13
US-08-934-915-7
Sequence 7, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-7

Query Match 39.5%; Score 47; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 0.85;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 NTMHYTNMTHIYI 16
| | | | | | | | | |
DB 7 NTMDYVWTHIYL 19

RESULT 14
US-09-000-094-46
Sequence 46, Application US/09000094
Patent No. 6365160
GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Bridgid
COX, John Cooper
FRAZER, Ian
MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
HOLLAND
EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPEPTIDE CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
TYPE: amino acid

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;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-000-094-46

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Query Match	39.58;	Score 47;	DB 4;	Length 1587;
Best Local Similarity	53.88;	Pred. NO. 97;		
Matches	7;	Conservative	2;	Mismatches 4;
				Indels 0;
				Gaps 0;

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QY      4 NTMHYTNWTHIYI 16
          ||| | | :|:
Db     165 NTMDYVWVTDVYV 177
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RESULT 15
dimeric-glycoprotein-receptor-extracellular
; Sequence 2, Application US/08474986
; Patent No. 6372711
GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: kelth

APPLICANT: Kelton, Christie Ann
Schwickhardt, Rene Lynn
Cheng, Shirley Vui Yen
Nugent, No. 637271leen Patrice
TITLE OF INVENTION: Human Follicle Stimulating
Hormone Receptor

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephan P. Williams,

STREET: Exchange Place, 37th floor
CITY: Boston

STATE: MA

COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX

OPERATING SYSTEM: MS-DOS version 4.0

SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,986

FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA: 07/05/00 000

APPLICATION NUMBER: 07/670,085

FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Williams, Stephan P.
REGISTRATION NUMBER: 39546

REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/2522
PER COMMUNICATION INFORMATION

TELEPHONE: (617) 733-1300

TELEPHONE: (617) 723-13
TELEFAX: (617) 723-8923

SEQUENCE CHARACTERISTICS.

LENGTH: 695

TOPOLOGY: Linear

TOPOLOGY: Linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY:	signal sequence
-----------	-----------------

NAME/KEY: signal sequence
LOCATION: -17 to -1
IDENTIFICATION METHOD: hydrophobic

IDENTIFICATION METHOD

NAME/KEY: putative amino-terminal extracellular domain
LOCATION: 1 to 349

IDENTIFICATION METHOD: similarity with other

dimeric-glycoprotein-receptor-extracellular

QY	4	NTMHTNWTHTIYIC	17
		:	
Db	6	NS, HYDROPHILIC	19

Search completed: January 14, 2003, 18:41:31
Job time : 15 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw.model

Run on: January 14, 2003, 18:39:58 ; Search time 11 Seconds
(without alignments)
33.511 Million cell updates/sec

Title: US-09-828-645-1

Perfect score: 119

Sequence: 1 DICTMYHTNWTHTIYCEE 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	43.7	334	10	US-09-886-055-365
2	50	42.0	436	10	US-09-925-300-1640
3	43	36.1	87	10	US-09-925-301-1125
4	43	36.1	313	10	US-09-788-626-7
5	43	36.1	314	10	US-09-886-055-141
6	42.5	33.7	135	10	US-09-864-761-9255
7	42	33.3	162	10	US-09-747-155-211
8	42	33.3	309	10	US-09-788-626-16
9	42	35.3	340	10	US-09-886-055-465
10	41	34.5	305	10	US-09-761-288-86
11	41	34.5	311	10	US-09-886-055-419
12	41	34.5	640	9	US-09-983-204-16
13	41	34.5	656	9	US-10-133-157-5
14	41	34.5	656	10	US-09-799-777-4
15	40.5	34.0	52	10	US-09-864-761-44604
16	40.5	34.0	241	9	US-09-738-626-6844
17	40.5	34.0	310	10	US-09-886-055-485
18	40	33.6	10	10	US-09-753-126-22
19	40	33.6	10	10	US-09-753-126-139

20	40	33.6	10	10	US-09-753-126-140	Sequence 140, App
21	40	33.6	216	10	US-09-747-155-49	Sequence 49, Appl
22	40	33.6	238	10	US-09-729-835-80	Sequence 80, Appl
23	40	33.6	309	10	US-09-886-055-383	Sequence 383, App
24	40	33.6	310	10	US-09-886-055-153	Sequence 153, App
25	40	33.6	333	10	US-09-771-209-71	Sequence 71, Appl
26	40	33.6	336	10	US-09-747-804-1	Sequence 1, Appl
27	40	33.6	419	12	US-10-005-202-2	Sequence 2, Appl
28	40	33.6	477	10	US-09-966-147-4	Sequence 4, Appl
29	40	33.6	525	10	US-09-871-503-2	Sequence 2, Appl
30	40	33.6	525	10	US-09-940-919-2	Sequence 2, Appl
31	40	33.6	822	10	US-09-966-147-2	Sequence 2, Appl
32	40	33.6	847	10	US-09-924-859A-5	Sequence 5, Appl
33	40	33.6	1350	10	US-09-893-238-17	Sequence 17, Appl
34	39.5	33.2	495	10	US-09-776-865-4	Sequence 4, Appl
35	39.5	33.2	495	10	US-09-915-181A-7	Sequence 7, Appl
36	39.5	33.2	536	10	US-09-776-865-2	Sequence 2, Appl
37	39	32.8	46	9	US-09-975-143-19	Sequence 19, Appl
38	39	32.8	160	10	US-09-970-711-38	Sequence 38, Appl
39	39	32.8	161	10	US-09-747-155-321	Sequence 321, App
40	39	32.8	161	10	US-09-747-155-323	Sequence 323, App
41	39	32.8	255	10	US-09-529-063-67	Sequence 67, Appl
42	39	32.8	281	10	US-09-864-761-43213	Sequence 43213, A
43	39	32.8	307	10	US-09-071-838-13	Sequence 13, Appl
44	39	32.8	338	10	US-09-886-055-427	Sequence 427, App
45	39	32.8	777	12	US-10-052-586-348	Sequence 348, App

ALIGNMENTS

RESULT 1

US-09-886-055-365

; Sequence 365, Application US/09886055

; Patent No. US20020132273A1

; GENERAL INFORMATION:

; APPLICANT: STRYER, LUBERT

; APPLICANT: ZOZULYA, SERGEY

; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND

; FILE REFERENCE: 078003-0277150

; CURRENT APPLICATION NUMBER: US/09/886,055

; CURRENT FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: 60/213,812

; PRIOR FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 522

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 365

; LENGTH: 334

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-886-055-365

Query Match 43.7%; Score 52; DB 10; Length 334;

Best Local Similarity 43.8%; Pred. No. 1.9;

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 ICNTMYHTNWTHTIYCEE 17

Db 146 VCRPLHYTLMHILHC 161

RESULT 2

US-09-925-300-1640

; Sequence 1640, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; APPLICANT: Steve Ruben

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

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; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1640

Query Match
Best Local Similarity 42.0%; Score 50; DB 10; Length 436;
Best Local Similarity 47.4%; Pred. No. 4.7;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DICTMHYNTWTHIYCEE 19
||| :||| :|||
Db 299 DIFPARHYSNMTVILKE 317

RESULT 3
US-09-925-301-1125
; Sequence 1125, Application US/09925301
; Patent No. US2002052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1125
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1125

Query Match
Best Local Similarity 36.1%; Score 43; DB 10; Length 87;
Best Local Similarity 46.2%; Pred. No. 9.8;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 CNTMHYNTWTHIY 15
||| :||| :|||
Db 22 CNDMPFYMTWLY 34

RESULT 4
US-09-788-626-7
; Sequence 7, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125,401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-788-626-7

Query Match
36.1%; Score 43; DB 10; Length 313;

Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 3 CNT-----MHTNW 11
||| :||| :|||
Db 142 CNETKLVYQYHNTW 156

RESULT 5
US-09-886-055-141
; Sequence 141, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRIER, LOBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-141

Query Match
Best Local Similarity 36.1%; Score 43; DB 10; Length 314;
Best Local Similarity 37.5%; Pred. No. 34;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 ICNTMHYNTWTHIYC 17
||| :||| :|||
Db 124 VCNPLHYTTMTTRVC 139

RESULT 6
US-09-864-761-39255
; Sequence 39255, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 4917
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39255
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005815.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EST_HUMAN HIT: BF738207.1, EVALUO 9.10e+00
; OTHER INFORMATION: SWISSPROT HIT: P32588, EVALUO 1.50e+00
US-09-864-761-39255

Query Match          35.7%; Score 42.5; DB 10; Length 135;
Best Local Similarity 38.9%; Pred. No. 18;
Matches 7; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 1 DICTMHTMHTHTIYC 18
      ||| :||| :||| :|||
Db 93 NICTIIPHTM-KHVLCE 109

RESULT 7
US-09-747-155-211
; Sequence 211, Application US/09747155
; Patent No. US20020151692A1
; GENERAL INFORMATION:
; APPLICANT: Rouquier, Sylvie
; TITLE OF INVENTION: No. US20020151692A1 Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 19904-008 (C009B834US)
; CURRENT APPLICATION NUMBER: US/09/747,155
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,746
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 431
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 211
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Gorilla gorilla
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(487)
; OTHER INFORMATION: Taxon = 9593; gene = GGO100; Accession DDBJ/EMBL/Genbank = AF1797
US-09-747-155-211

Query Match          35.3%; Score 42; DB 10; Length 162;
Best Local Similarity 23.3%; Pred. No. 25;
Matches 7; Conservative 6; Mismatches 3; Indels 14; Gaps 1;
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QY 2 ICNTMHTMHTHTIYC 17
      ||| :||| :||| :|||
Db 3 ICPLHTYIMDONTCTQLAVISMSSFLC 32

RESULT 8
US-09-788-626-16
; Sequence 16, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-788-626-16

Query Match          35.3%; Score 42; DB 10; Length 309;
Best Local Similarity 37.5%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 ICNTMHTMHTHTIYC 17
      ||| :||| :||| :|||
Db 117 ILNDSHYADWVPMFLC 132

RESULT 9
US-09-886-055-465
; Sequence 465, Application US/09886055
; Patent No. US2002013273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 465
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-465

Query Match          35.3%; Score 42; DB 10; Length 340;
Best Local Similarity 43.8%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 ICNTMHTMHTHTIYC 17
      ||| :||| :||| :|||
Db 147 ICPLHTYIMHPOLC 162

RESULT 10
US-09-761-288-86
; Sequence 86, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
```

APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Li, Li
TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam
FILE REFERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/177,839
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/176,134
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/175,989
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,253
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,227
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/220,590
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 86
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-09-761-288-86

Query Match 34.5%; Score 41; DB 10; Length 305;
Best Local Similarity 37.5%; Pred. No. 64;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 2 ICNTMHTNMTHTIYC 17
|| :||:| :||:|
DB 126 ICIPLHYSNVMNMKVC 141

RESULT 11
US-09-886-055-419
; Sequence 419, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZOLYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 419
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-419

Query Match 34.5%; Score 41; DB 10; Length 311;
Best Local Similarity 29.4%; Pred. No. 65;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 2 ICNTMHTNMTHTIYICE 18
|| :||:| :||:|
DB 126 VCRPLHYMAIMPHLCO 142

RESULT 12
US-09-983-204-16
; Sequence 16, Application US/09983204
; Patent No. US20020173000A1
; GENERAL INFORMATION:
; APPLICANT: RENARD, STEPHANE
; APPLICANT: BESNARD, FRANCOIS
; APPLICANT: GRAHAM, DAVID
; TITLE OF INVENTION: SODIUM CHANNEL RECEPTOR
; FILE REFERENCE: 07586.0010
; CURRENT APPLICATION NUMBER: US/09/983,204
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/424,666
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02884
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 97401196.7
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: HNNCHB
US-09-983-204-16

Query Match 34.5%; Score 41; DB 9; Length 640;
Best Local Similarity 38.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 CNTMHTNMTHTIY 15
|| :||:| :||:|
DB 415 CNNDPDPMAHCY 427

RESULT 13
US-10-133-157-5
; Sequence 5, Application US/10133157
; Publication No. US20020184054A1
; GENERAL INFORMATION:
; APPLICANT: CALLAMARAS, NICHOLAS
; APPLICANT: CHANG, HONG
; TITLE OF INVENTION: HIGH THROUGHPUT CELL-BASED ASSAY FOR MONITORING SODIUM
; TITLE OF INVENTION: CHANNEL ACTIVITY AND DISCOVERY OF SALTY TASTE
; TITLE OF INVENTION: MODULATING COMPOUNDS
; FILE REFERENCE: 078003-0280790
; CURRENT APPLICATION NUMBER: US/10/133,157
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: 60/287,413
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-133-157-5

Query Match 34.5%; Score 41; DB 9; Length 640;
Best Local Similarity 38.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 CNTMHTNMTHTIY 15
|| :||:| :||:|
DB 415 CNNDPDPMAHCY 427

RESULT 14
US-09-799-777-4
; Sequence 4, Application US/09799777
; Patent No. US20020091244A1

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PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 44604
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF241727.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.55
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.47
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.75
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.2
OTHER INFORMATION: SWISSPROT HIT: P41732, EVALUATION: 1.00e-28
OTHER INFORMATION: EST_HUMAN HIT: BE741256.1, EVALUATION: 2.00e-27
US-09-864-761-44604

Query Match          34.0%; Score 40.5; DB 10; Length 52;
Best Local Similarity 47.1%; Pred. No. 13;
Matches      8; Conservative      1; Mismatches      7; Indels      1; Gaps      1

3 CNTMTATTNN-THIYICE 18
4 CGVQNTNNMSTSYFLE 20

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:38:33 ; Search time 29 Seconds
(Without alignments)
134.996 Million cell updates/sec

Title: US-09-828-645-1

Perfect score: 119
Sequence: 1 DICNTMHTMTWTHIYCEE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rhodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvrius:*
17: sp_bacteriap:*
18: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	359	12	0918T0 human papill
2	119	100.0	361	12	0918U7 human papill
3	119	100.0	361	12	0918U5 human papill
4	119	100.0	361	12	0918U3 human papill
5	119	100.0	361	12	0918U1 human papill
6	119	100.0	365	12	0918U2 human papill
7	119	100.0	365	12	0918U4 human papill
8	119	100.0	365	12	0918U3 human papill
9	119	100.0	365	12	0918U7 human papill
10	119	100.0	365	12	0918U5 human papill
11	119	100.0	365	12	0918U3 human papill
12	119	100.0	365	12	0918U1 human papill
13	119	100.0	365	12	0918U2 human papill
14	119	100.0	365	12	0918U4 human papill
15	119	100.0	365	12	0918U3 human papill
16	119	100.0	361	12	0918T8 human papill

17	110	92.4	365	12	091V72 human papill
18	107	89.9	365	12	091E80 human papill
19	107	89.9	365	12	091W04 human papill
20	64.5	54.2	370	12	081967 human papill
21	64	53.8	314	5	091E71 leishmania
22	62	52.1	377	12	091W03 human papill
23	60	50.4	359	12	091R56 human papill
24	60	50.4	359	12	091R57 human papill
25	59	49.6	380	12	091W07 human papill
26	57	47.9	368	12	090726 human papill
27	54	45.4	376	12	037387 common chim
28	53	44.5	469	12	056937 human papill
29	51	42.9	350	12	082008 human papill
30	50	42.0	278	4	091U05 human papill
31	50	42.0	284	4	096BV3 human papill
32	50	42.0	478	12	056943 human papill
33	48	40.3	587	5	0960P7 drosophila
34	47.5	39.9	702	15	090C07 human endog
35	47	39.5	368	12	091YPI human papill
36	47	39.5	444	12	056955 human papill
37	47	39.5	453	10	091U91 arabidopsi
38	47	39.5	776	12	P88981 murid herpe
39	46.5	39.1	519	10	091FX7 arabidopsi
40	46.5	39.1	676	16	08X0P3 ralsionia s
41	46	38.7	227	15	011515 human immun
42	46	38.7	288	10	09AVH4 pisum sativ
43	46	38.7	311	11	08VGX0 mus muscula
44	46	38.7	311	11	08VFA7 mus muscula
45	46	38.7	311	11	08VFA6 mus muscula

ALIGNMENTS

RESULT 1	0918T0	PRELIMINARY:	PRT:	359 AA.
ID	0918T0			
AC	0918T0:			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	E2 protein (Fragment).			
GN	E2.			
OS	Human papillomavirus type 16.			
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;			
OC	Papillomavirus.			
OX	NCBI_TaxID=10581;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HPV16E2C8;			
RA	Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;			
RT	*Sequence variation and physical state of human Papillomavirus type 16			
RT	cervical cancer isolates from Australia and New Caledonia.";			
RL	Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AF407221; A01407.1; -			
DR	InterPro: IPR000427; E2_C.			
DR	InterPro: IPR01866; E2_N.			
DR	Pfam: PF00511; E2_C; 1.			
DR	Pfam: PF00508; E2_N; 1.			
DR	ProDom: PD000672; E2_C; 1.			
DR	ProDom: PD000678; E2_N; 1.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	359 AA;	41122 MW;	375DC218679CEA89 CRC64;
Query Match		100.0%;	Score 119;	DB 12; Length 359;
Best local Similarity		100.0%;	Pred. No. 8.6e-11;	
Matches	19;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
QY	1 DICNTMHTMTWTHIYCEE 19			
DB	121 DICNTMHTMTWTHIYCEE 139			

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RESULT 2
Q91807 PRELIMINARY; PRT; 361 AA.
ID 091807;
AC 091807;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E2 protein (Fragment).
GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC1;
RA "Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407214; AAL01386.1; -.
DR InterPro; IPR000427; E2_C.
DR InterPro; IPR001866; E2_N.
DR Pfam; PF00511; E2_C; 1.
DR Pfam; PF00508; E2_N; 1.
DR Prodom; PD000672; E2_C; 1.
DR Prodom; PD000678; E2_N; 1.
FT NON_TER 1
FT NON_TER 361
SQ SEQUENCE 361 AA; 41335 MW; 87D0B9CEBCA9558D CRC64;

Query Match 100.0%; Score 119; DB 12; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIGNTMHYTNWTHIYCEE 19
Db 121 DIGNTMHYTNWTHIYCEE 139

RESULT 3
Q91805 PRELIMINARY; PRT; 361 AA.
ID 091805;
AC 091805;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E2 protein (Fragment).
GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC2;
RA "Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407215; AAL01389.1; -.
DR InterPro; IPR000427; E2_C.
DR InterPro; IPR001866; E2_N.
DR Pfam; PF00511; E2_C; 1.
DR Pfam; PF00508; E2_N; 1.
DR Prodom; PD000672; E2_C; 1.
DR Prodom; PD000678; E2_N; 1.
FT NON_TER 1
FT NON_TER 361
SQ SEQUENCE 361 AA; 41395 MW; 9CD109CEBCA9558D CRC64;

Query Match 100.0%; Score 119; DB 12; Length 361;
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Best Local Similarity 100.0%; Pred. No. 8.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIGNTMHYTNWTHIYCEE 19
Db 121 DIGNTMHYTNWTHIYCEE 139

RESULT 4
Q91803 PRELIMINARY; PRT; 361 AA.
ID 091803;
AC 091803;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E2 protein (Fragment).
GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC3;
RA "Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407216; AAL01392.1; -.
DR InterPro; IPR000427; E2_C.
DR InterPro; IPR001866; E2_N.
DR Pfam; PF00511; E2_C; 1.
DR Pfam; PF00508; E2_N; 1.
DR Prodom; PD000672; E2_C; 1.
DR Prodom; PD000678; E2_N; 1.
FT NON_TER 1
FT NON_TER 361
SQ SEQUENCE 361 AA; 41356 MW; B973EA921D39BD97 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIGNTMHYTNWTHIYCEE 19
Db 121 DIGNTMHYTNWTHIYCEE 139

RESULT 5
Q91801 PRELIMINARY; PRT; 361 AA.
ID 091801;
AC 091801;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E2 protein (Fragment).
GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC4;
RA "Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407217; AAL01395.1; -.
DR InterPro; IPR000427; E2_C.
DR InterPro; IPR001866; E2_N.
DR Pfam; PF00511; E2_C; 1.
DR Pfam; PF00508; E2_N; 1.
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ed Jan 15 11:37:14 2003

DR ProDom: PD000672; E2_C: 1.
 DR ProDom: PD000678; E2_N: 1.
 FT NON_TER 1
 FT NON_TER 361
 SQ SEQUENCE 361 AA; 41394 MW; ESE738AB8BAEF4C9 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
 Best Local Similarity 100.0%; Pred. No. 8.7e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTNMTNMTNTHIYCEE 19
 |||
 Db 121 DICTNMTNMTNTHIYCEE 139

RESULT 6
 Q9E842 PRELIMINARY; PRT; 365 AA.

AC Q9E842; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE E2 protein variant.
 GN E2.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DAG1;
 RX MEDLINE=20495818; PubMed=11040943;
 RA Graham D.A., Herington C.S.;
 RT "HPV-16 E2 gene disruption and sequence variation in CIN 3 lesions and
 RT invasive squamous cell carcinomas of the cervix: relation to numerical
 RT chromosome abnormalities.";
 RT Mol. Pathol. 53:201-206(2000).
 RL EMBL: AF193425; ANG31352.1; -.
 DR HSSP: P17383; IDHM.
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00511; E2_C: 1.
 DR Pfam: PF00508; E2_N: 1.
 DR ProDom: PD000672; E2_C: 1.
 DR ProDom: PD000678; E2_N: 1.
 DR ProDom: PD000678; E2_N: 1.
 SQ SEQUENCE 365 AA; 41805 MW; A647FDDEE056C0D CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
 Best Local Similarity 100.0%; Pred. No. 8.8e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTNMTNMTNTHIYCEE 19
 |||
 Db 124 DICTNMTNMTNTHIYCEE 142

RESULT 7
 Q9E841 PRELIMINARY; PRT; 365 AA.

AC Q9E841; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE E2 protein variant.
 GN E2.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DAG2;
 RX MEDLINE=20495818; PubMed=11040943;

RA Graham D.A., Herington C.S.;
 RT "HPV-16 E2 gene disruption and sequence variation in CIN 3 lesions and
 RT invasive squamous cell carcinomas of the cervix: relation to numerical
 RT chromosome abnormalities.";
 RT Mol. Pathol. 53:201-206(2000).
 RL EMBL: AF193426; ANG31353.1; -.
 DR HSSP: P17383; IDHM.
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00511; E2_C: 1.
 DR Pfam: PF00508; E2_N: 1.
 DR ProDom: PD000672; E2_C: 1.
 DR ProDom: PD000678; E2_N: 1.
 DR ProDom: PD000678; E2_N: 1.
 SQ SEQUENCE 365 AA; 41801 MW; 24682DDE132B7543 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
 Best Local Similarity 100.0%; Pred. No. 8.8e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTNMTNMTNTHIYCEE 19
 |||
 Db 124 DICTNMTNMTNTHIYCEE 142

RESULT 8
 Q9E839 PRELIMINARY; PRT; 365 AA.

AC Q9E839; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE E2 protein variant.
 GN E2.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DAG6;
 RX MEDLINE=20495818; PubMed=11040943;
 RA Graham D.A., Herington C.S.;
 RT "HPV-16 E2 gene disruption and sequence variation in CIN 3 lesions and
 RT invasive squamous cell carcinomas of the cervix: relation to numerical
 RT chromosome abnormalities.";
 RT Mol. Pathol. 53:201-206(2000).
 RL EMBL: AF193430; ANG31357.1; -.
 DR HSSP: P17383; IDHM.
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00511; E2_C: 1.
 DR Pfam: PF00508; E2_N: 1.
 DR ProDom: PD000672; E2_C: 1.
 DR ProDom: PD000678; E2_N: 1.
 DR ProDom: PD000678; E2_N: 1.
 SQ SEQUENCE 365 AA; 41809 MW; 3EA67F918055C020 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
 Best Local Similarity 100.0%; Pred. No. 8.8e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTNMTNMTNTHIYCEE 19
 |||
 Db 124 DICTNMTNMTNTHIYCEE 142

RESULT 9
 Q9YV76 PRELIMINARY; PRT; 365 AA.

AC Q9YV76; 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Regulatory protein E2.

GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
ON NCBI_Taxid=10581;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-H990;
RX MEDLINE=99226956; PubMed=10211974;
RA Veress G., Szarka K., Dong X.P., Gergely L., Pfister H.;
RT "Functional significance of sequence variation in the E2 gene and the
RT long control region of human papillomavirus type 16.";
RL J. Gen. Virol. 80:1035-1043(1999).
DR EMBL: AF067031; AAD03827.1; -
DR HSSP: P17383; IDHM.
DR InterPro: IPR000427; E2_C.
DR InterPro: IPR001866; E2_N.
DR Pfam: PF00511; E2_C; 1.
DR Pfam: PF00508; E2_N; 1.
DR ProDom: PD000672; E2_C; 1.
DR ProDom: PD000678; E2_N; 1.
SQ SEQUENCE 365 AA; 41841 MW; 2745A882B246E112 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
Best Local Similarity 100.0%; Pred. No. 8.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DICTNMYTHYTHIYCEE 19
Db 124 DICTNMYTHYTHIYCEE 142

RESULT 10
O9YV75 PRELIMINARY; PRT; 365 AA.
ID O9YV75;
AC O9YV75;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Regulatory protein E2.
GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
ON NCBI_Taxid=10581;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-H955;
RX MEDLINE=99226956; PubMed=10211974;
RA Veress G., Szarka K., Dong X.P., Gergely L., Pfister H.;
RT "Functional significance of sequence variation in the E2 gene and the
RT long control region of human papillomavirus type 16.";
RL J. Gen. Virol. 80:1035-1043(1999).
DR EMBL: AF067032; AAD03828.1; -
DR HSSP: P17383; IDHM.
DR InterPro: IPR000427; E2_C.
DR InterPro: IPR001866; E2_N.
DR Pfam: PF00511; E2_C; 1.
DR Pfam: PF00508; E2_N; 1.
DR ProDom: PD000672; E2_C; 1.
DR ProDom: PD000678; E2_N; 1.
SQ SEQUENCE 365 AA; 41816 MW; 3EB2EDDF132B7112 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
Best Local Similarity 100.0%; Pred. No. 8.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DICTNMYTHYTHIYCEE 19
Db 124 DICTNMYTHYTHIYCEE 142

RESULT 11

O9YV74 PRELIMINARY; PRT; 365 AA.
ID O9YV74;
AC O9YV74;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Regulatory protein E2.
GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
ON NCBI_Taxid=10581;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-H982;
RX MEDLINE=99226956; PubMed=10211974;
RA Veress G., Szarka K., Dong X.P., Gergely L., Pfister H.;
RT "Functional significance of sequence variation in the E2 gene and the
RT long control region of human papillomavirus type 16.";
RL J. Gen. Virol. 80:1035-1043(1999).
DR EMBL: AF067033; AAD03829.1; -
DR HSSP: P17383; IDHM.
DR InterPro: IPR000427; E2_C.
DR InterPro: IPR001866; E2_N.
DR Pfam: PF00511; E2_C; 1.
DR Pfam: PF00508; E2_N; 1.
DR ProDom: PD000672; E2_C; 1.
DR ProDom: PD000678; E2_N; 1.
SQ SEQUENCE 365 AA; 41831 MW; 17B9CC9470D3376 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
Best Local Similarity 100.0%; Pred. No. 8.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DICTNMYTHYTHIYCEE 19
Db 124 DICTNMYTHYTHIYCEE 142

RESULT 12
O9YIV0 PRELIMINARY; PRT; 365 AA.
ID O9YIV0;
AC O9YIV0;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Regulatory protein E2 (E2 protein variant).
GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
ON NCBI_Taxid=10581;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-H050, AND H936;
RA Veress G., Szarka K., Dong X.-P., Gergely L., Pfister H.;
RT "Sequence variation in the E2 gene and in the long control region of
RT human papillomavirus type 16.";
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-16M12E;
RA Flores E.R., Nelson J.H., Lambert P.F.;
RT "Establishment of the human papillomavirus life cycle in an
RT immortalized human foreskin keratinocyte cell line.";
RT Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN-DAG3;
RX MEDLINE=20495818; PubMed=11040943;
RA Graham D.A., Herrington C.S.;
RT "HPV-16 E2 gene disruption and sequence variation in CIN 3 lesions and
RT invasive squamous cell carcinomas of the cervix: relation to numerical

RT Chromosome abnormalities.
 RL Mol. Pathol. 53:201-206(2000).
 DR EMBL: AF067030; AAD03826.1; -
 DR EMBL: AF067029; AAD03825.1; -
 DR EMBL: AF125673; AAD33255.1; -
 DR EMBL: AF193427; AAG31354.1; -
 DR HSSP: P17383; IDHM.
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00511; E2_C; 1.
 DR Pfam: PF00508; E2_N; 1.
 DR ProDom: PD000672; E2_C; 1.
 DR ProDom: PD000678; E2_N; 1.
 SO SEQUENCE 365 AA; 41815 MW; 24682DDE132B7112 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
 Best Local Similarity 100.0%; Pred. No. 8.8e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTMHTMTHIYCEE 19
 DB 124 DICTMHTMTHIYCEE 142

RESULT 13
 Q9YV73 PRELIMINARY; PRT; 365 AA.
 ID Q9YV73
 AC Q9YV73
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Regulatory protein E2 (E2 protein variant).
 GN E2.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Veress G., Szarka K., Dong X.-P., Gergely L., Pfister H.;
 RT "Sequence variation in the E2 gene and in the long control region of
 RT human papillomavirus type 16."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RC SEQUENCE FROM N.A.
 RX STRAIN=DAG4;
 RA MEDLINE=20495818; PubMed=11040943;
 RA Graham D.A., Herrington C.S.;
 RT "HPV-16 E2 gene disruption and sequence variation in CIN 3 lesions and
 RT invasive squamous cell carcinomas of the cervix: relation to numerical
 RT chromosome abnormalities."
 RL Mol. Pathol. 53:201-206(2000).
 DR EMBL: AF067034; AAD03830.1; -
 DR EMBL: AF193428; AAG31355.1; -
 DR HSSP: P17383; IDHM.
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00511; E2_C; 1.
 DR Pfam: PF00508; E2_N; 1.
 DR ProDom: PD000672; E2_C; 1.
 DR ProDom: PD000678; E2_N; 1.
 SO SEQUENCE 365 AA; 41830 MW; 2B78DCC2DC450C8 CRC64;

Query Match 100.0%; Score 119; DB 12; Length 365;
 Best Local Similarity 100.0%; Pred. No. 8.8e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 Q918T5 PRELIMINARY; PRT; 356 AA.
 ID Q918T5
 AC Q918T5
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE E2 protein (Fragment).
 GN E2.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=HPV16E2CC6;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human Papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF407219; AAL01401.1; -
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00511; E2_C; 1.
 DR Pfam: PF00508; E2_N; 1.
 DR ProDom: PD000672; E2_C; 1.
 DR ProDom: PD000678; E2_N; 1.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 356 AA; 40804 MW; 5C0A1B6BE794EEE CRC64;

Query Match 95.0%; Score 113; DB 12; Length 356;
 Best Local Similarity 94.7%; Pred. No. 7.5e-10;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DICTMHTMTHIYCEE 19
 DB 118 DICTMHTMTHIYCEE 136

RESULT 15
 Q918T3 PRELIMINARY; PRT; 356 AA.
 ID Q918T3
 AC Q918T3
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE E2 protein (Fragment).
 GN E2.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=HPV16E2CC7;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human Papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF407220; AAL01404.1; -
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00511; E2_C; 1.
 DR Pfam: PF00508; E2_N; 1.
 DR ProDom: PD000672; E2_C; 1.
 DR ProDom: PD000678; E2_N; 1.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 356 AA; 40695 MW; 41BAADF8B6A0110 CRC64;

Query Match 95.0%; Score 113; DB 12; Length 356;
 Best Local Similarity 94.7%; Pred. No. 7.5e-10;

Matches	18;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	DICNTMHTNNTHTIYICEE	19						
Db	118	DICNTMHTNNTMKNKHTIYICEE	136						

Search completed: January 14, 2003, 18:40:48
Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:38:58 : Search time 15 seconds
(without alignments)
121.770 Million cell updates/sec

Title: US-09-828-645-1

Perfect score: 119

Sequence: 1 DICNTMHTNMTHTIYCEE 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	365	1 W2WLHS	E2 protein - human
2	87	73.1	367	1 W2WL35	E2 protein - human
3	87	73.1	367	2 S36524	E2 protein - human
4	79	66.4	372	1 W2WL31	E2 protein - human
5	72	60.5	358	1 W2WL58	E2 protein - human
6	66	55.5	353	1 W2WL33	E2 protein - human
7	64	53.8	377	1 W2WL31	E2 protein - human
8	62	52.1	398	1 W2WL42	E2 protein - human
9	58.5	49.2	368	2 S36576	E2 protein - human
10	58	48.7	394	2 S36512	E2 protein - human
11	55	46.2	370	2 S36558	E2 protein - human
12	55	46.2	375	2 S36587	E2 protein - human
13	52.5	44.1	377	1 W2WL13	E2 protein - human
14	52	43.7	367	1 W2WL11	E2 protein - human
15	51	42.9	366	1 W2WL11	E2 protein - human
16	47	39.5	358	1 W2WL51	E2 protein - human
17	47	39.5	368	1 W2WL6	E2 protein - human
18	46	38.7	370	1 W2WL39	E2 protein - human
19	46	38.7	1080	2 T19048	E2 protein - human
20	45	37.8	154	2 S58070	probable Pro-x car
21	45	37.8	155	2 T28164	probable Olfactory
22	45	37.8	321	2 S65225	hypothetical prote
23	45	37.8	345	2 S36518	probable membrane
24	45	37.8	382	2 S36476	E2 protein - human
25	45	37.8	383	1 S15624	E2 protein - human
26	45	37.8	388	1 S36500	E2 protein - human
27	44	37.0	99	2 AH3429	transposase BMEL14
28	44	37.0	158	2 T26692	hypothetical prote
29	43	36.1	101	2 AC3467	sarcosine oxidase

30	43	36.1	152	1 MNN22G	gene 2 protein - p
31	43	36.1	296	1 A69693	integrase/recombin
32	43	36.1	334	1 W2WL84	E2 protein - bovin
33	43	36.1	365	2 F88449	protein F54D8.4 (i
34	43	36.1	375	2 S36547	E2 protein - human
35	43	36.1	768	2 B97083	glycosyltransferas
36	43	36.1	929	2 T17392	vrll protein - dic
37	43	36.1	1301	1 A41622	protein-tyrosine-p
38	43	36.1	1529	2 T02730	rna-directed dna p
39	42.5	35.7	407	2 T08732	hypothetical prote
40	42.5	35.7	461	2 T16161	hypothetical prote
41	42.5	35.7	560	2 T16833	hypothetical prote
42	42.5	35.7	1031	2 T43458	hypothetical prote
43	42	35.3	282	2 JC5677	RNA4 protein - bee
44	42	35.3	282	2 C44503	p31 protein - bee
45	42	35.3	305	2 T23022	hypothetical prote

ALIGNMENTS

RESULT 1
W2WLHS
E2 protein - human papillomavirus type 16
C:Species: human papillomavirus type 16
C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 20-Aug-1999
C:Accession: A03669; T10429
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Roweckamp, W.G.
Virology 145, 181-185, 1985
A>Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03669
A:Molecule type: DNA
A:Residues: 1-365 <SEE>
A:Cross-references: GB:K02718; MID:9333031; PIDN:AAA46941.1; PID:9333035
R.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A>Title: A negative element in the human poapillomavirus type 16 genome acts at the 1
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-365 <KEN>
A:Cross-references: EMBL:K02718; NID:9333031; PIDN:AAA46941.1; PID:9333035
C:Genetics:
A:Gene: E2
C:Superfamily: papillomavirus E2 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 100.0%; Score 119; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DICNTMHTNMTHTIYCEE 19
Db 124 DICNTMHTNMTHTIYCEE 142

RESULT 2
W2WL35
E2 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A>Note: host Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
R:March, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A>Title: The phylogenetic relationship and complete nucleotide sequence of human papi
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-367 <MAR>

A:Cross-references: GB:M74117; NID:g333050; PIDN:AAA46969.1; PID:g333054
C:Superfamily: papillomavirus E2 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 73.1%; Score 87; DB 1; Length 367;
Best Local Similarity 87.5%; Pred. No. 4.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 NTMHTNMTHTIYICEE 19
|||||
Db 128 NTMHTNMTHTIYILED 143

RESULT 3

S36524
E2 protein - human papillomavirus type 35H
C:Species: human papillomavirus type 35H
C:Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S36524
R:Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36524
A:Molecule type: DNA
A:Residues: 1-367

A:Cross-references: EMBL:X74477
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E2 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 73.1%; Score 87; DB 2; Length 367;
Best Local Similarity 87.5%; Pred. No. 4.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 NTMHTNMTHTIYICEE 19
|||||
Db 128 NTMHTNMTHTIYILED 143

RESULT 4

W2ML31
E2 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C:Accession: D32444
R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: D32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-372 <GO>

A:Cross-references: GB:J04353; NID:g333048; PIDN:AAA46953.1; PID:g459919
C:Superfamily: papillomavirus E2 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 66.4%; Score 79; DB 1; Length 372;
Best Local Similarity 70.6%; Pred. No. 0.00063;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DICNTMHTNMTHTIYC 17
|:|||||
Db 124 DVHNTMHTNMKFYLC 140

RESULT 5

W2ML58
E2 protein - human papillomavirus type 58
C:Species: human papillomavirus type 58
A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
C:Accession: B36779
R:Kiril, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991

A:Title: Human papillomavirus type 58 DNA sequence.
A:Reference number: A36779; MUID:92024102; PMID:1656594
A:Accession: B36779
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <KIR>

A:Cross-references: GB:D90400; NID:g222386; PIDN:BA31848.1; PID:g3337101
C:Superfamily: papillomavirus E2 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 60.5%; Score 72; DB 1; Length 358;
Best Local Similarity 68.4%; Pred. No. 0.0061;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 DICNTMHTNMTHTIYICEE 19
|:|||||
Db 124 DKANTMDYTNNSEIYIEE 142

RESULT 6

W2ML33
E2 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A03670
R:Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33.
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03670
A:Molecule type: DNA
A:Residues: 1-553 <COL>

A:Cross-references: GB:M12732; NID:g333049; PIDN:AAA46961.1; PID:g463180
C:Superfamily: papillomavirus E2 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 55.5%; Score 66; DB 1; Length 353;
Best Local Similarity 75.0%; Pred. No. 0.044;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 NTMHTNMTHTIYICEE 19
|||||
Db 127 NTMDYTNNGEIYIIEE 142

RESULT 7

W2MLC1
E2 protein - pygmy chimpanzee papillomavirus (type 1)
C:Species: pygmy chimpanzee papillomavirus
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
C:Accession: D36818
R:van Ransst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker
Virology 190, 587-596, 1992
A:Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Com
A:Reference number: A42955; MUID:92391075; PMID:1325697
A:Accession: D36818
A:Molecule type: DNA
A:Residues: 1-377 <VAN>

A:Cross-references: EMBL:X62844; NID:g61010; PIDN:CAA44658.1; PID:g61014
C:Superfamily: papillomavirus E2 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 53.8%; Score 64; DB 1; Length 377;
Best Local Similarity 60.0%; Pred. No. 0.091;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 NTMHTNMTHTIYICEE 18
|:|||||
Db 127 NSMHTVLMKVIYVCE 141

RESULT 8
W2ML42

E2 protein - human papillomavirus type 42

C:Species: human papillomavirus type 42

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Feb-1997

C:Accession: B39451

R:Phillip, W.; Honore, N.; Sapp, M.; Cole, S.T.; Strebeck, R.E.

Virology 186, 331-334, 1992

A:Title: Human papillomavirus type 42: new sequence, conserved genome organization.

A:Reference number: A39451; MUID:92087479; PMID:1309278

C:Accession: B39451

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-398 <PHI>

A:Cross-References: GB:M73236

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 52.1%; Score 62; DB 1; Length 398;

Best Local Similarity 76.9%; Pred. No. 0.19;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NTMHYTNWTHIYI 16

DB 127 NAMHYTAWTYIYI 139

RESULT 9
S36576

E2 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36576

R:Deilus, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36576

A:Molecule type: DNA

A:Residues: 1-368

A:Cross-References: EMBL:X74481; NID:q397038; PIDN:CAAS2588.1; PID:q397042

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 49.2%; Score 58.5; DB 2; Length 368;

Best Local Similarity 61.1%; Pred. No. 0.55;

Matches 11; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 4 NTMHYTNWTHIYI ---CE 18

DB 127 NTMDYTNMKREIYLGECE 144

RESULT 10
S36512

E2 protein - human papillomavirus type 32

C:Species: human papillomavirus type 32

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36512

R:Deilus, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36512

A:Molecule type: DNA

A:Residues: 1-394

A:Cross-References: EMBL:X74475; NID:q396981; PIDN:CAAS2552.1; PID:q396985

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 48.7%; Score 58; DB 2; Length 394;
Best Local Similarity 69.2%; Pred. No. 0.69;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NTMHYTNWTHIYI 16
DB 127 NAMHYTAWTYIYI 139

RESULT 11
S36558

E2 protein - human papillomavirus type 40

C:Species: human papillomavirus type 40

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36558

R:Deilus, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36558

A:Molecule type: DNA

A:Residues: 1-370

A:Cross-References: EMBL:X74478; NID:q397014; PIDN:CAAS2570.1; PID:q397018

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 46.2%; Score 55; DB 2; Length 370;

Best Local Similarity 61.5%; Pred. No. 1.8;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 NTMHYTNWTHIYI 16

DB 127 NAMHYTAWTYIYI 139

RESULT 12
S36587

E2 protein - human papillomavirus type 7

C:Species: human papillomavirus type 7

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36587

R:Deilus, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36587

A:Molecule type: DNA

A:Residues: 1-375

A:Cross-References: EMBL:X74463; NID:q397060; PIDN:CAAS2479.1; PID:q397064

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 46.2%; Score 55; DB 2; Length 375;

Best Local Similarity 61.5%; Pred. No. 1.8;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 NTMHYTNWTHIYI 16

DB 127 NAMHYTAWTYIYI 139

RESULT 13
W2ML13

E2 protein - human papillomavirus type 13

C:Species: human papillomavirus type 13

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999

C:Accession: DA2955

R:van Ranst, M.; Fuse, A.; Fliten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker

Virology 190, 587-596, 1992

A:Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Com

A:Reference number: A42955; MUID:92391075; PMID:1325697

A:Accession: DA2955

A:Molecule type: DNA
A:Residues: 1-377 <VAN>

A:Cross-References: EMBL:X62843; NID:g60295; PIDN:CAA44650.1; PID:g60299

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match

Best Local Similarity 44.1%; Score 52.5; DB 1; Length 377;

Matches 9; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

OY 3 CNT--MHTNMTHTIYI 16

DB 123 CNTNRMQIVSWTITIV 139

RESULT 14

W2WL11

E2 protein - human papillomavirus type 11

C:Species: human papillomavirus type 11

C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 16-Jul-1999

C:Accession: A03668

R:Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.

Virolology 151, 124-130, 1986

A:Title: The nucleotide sequence and genome organization of human papilloma virus type 1

A:Reference number: A94336; MUID:86181601; PMID:3008427

A:Accession: A03668

A:Molecule type: DNA

A:Residues: 1-367 <DAR>

A:Cross-References: GB:M4119; NID:g333026; PIDN:AAA46930.1; PID:g496196

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match

Best Local Similarity 43.7%; Score 52; DB 1; Length 367;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 NTMHTNMTHTIYI 16

DB 127 NMVEYVWTHIYL 139

RESULT 15

W2WL11

E2 protein - rhesus papillomavirus (type 1)

C:Species: rhesus papillomavirus

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997

C:Accession: D38503

R:OSTROW, R.S.; Labresh, K.V.; Faras, A.J.

Virolology 181, 424-429, 1991

A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc

A:Reference number: A38503; MUID:91135018; PMID:1847267

A:Accession: D38503

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-366 <OST>

A:Cross-References: EMBL:M37717

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match

Best Local Similarity 42.9%; Score 51; DB 1; Length 366;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 NTMHTNMTHTIYI 16

DB 128 NTMEYVLMGHTIV 140

Search completed: January 14, 2003, 18:41:10
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:38:03 : Search time 11 Seconds
(without alignments)
71.641 Million cell updates/sec

Title: US-09-828-645-1
Perfect score: 119
Sequence: 1 DICNTMYNTMYICEE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	365	VE2_HPV16	P03120 human papill
2	87	73.1	367	VE2_HPV35	P27222 human papill
3	79	66.4	372	VE2_HPV31	P17383 human papill
4	72	60.5	358	VE2_HPV58	P26546 human papill
5	66	55.5	353	VE2_HPV33	P06423 human papill
6	64	53.8	377	VE2_PCPIV	Q02264 pygmy chimp
7	62	52.1	398	VE2_HPV42	P27223 human papill
8	58.5	49.2	368	VE2_HPV52	P36796 human papill
9	58	48.7	394	VE2_HPV32	P36791 human papill
10	55	46.2	370	VE2_HPV40	P36793 human papill
11	55	46.2	375	VE2_HPV07	P36779 human papill
12	52.5	44.1	377	VE2_HPV13	Q02263 human papill
13	52	43.7	367	VE2_HPV11	P04015 human papill
14	51	42.9	366	VE2_HPV1	P22156 rhesus papil
15	50	42.0	404	VE2_HPV60	Q08046 human papil
16	48	40.3	402	VE2_HPV65	Q07851 human papil
17	47	39.5	358	VE2_HPV51	P26547 human papil
18	47	39.5	368	VE2_HPV6A	Q84294 human papil
19	47	39.5	368	VE2_HPV6B	P03119 human papil
20	47	39.5	441	VE2_HPV38	Q08010 human papil
21	46	38.7	370	VE2_HPV39	P24830 human papil
22	46	38.7	509	VE2_HPV36	P50809 human papil
23	45	37.8	345	VE2_HPV34	P36792 human papil
24	45	37.8	382	VE2_HPV15	P36784 human papil
25	45	37.8	383	VE2_HPV57	P22155 human papil
26	45	37.8	388	VE2_HPV27	P36789 human papil
27	44	37.0	402	VE2_HPV55	Q08037 human papil
28	44	37.0	402	VE2_HPV04	Q07849 human papil
29	44	37.0	436	VE2_HPV22	P50768 human papil
30	44	37.0	663	VE2_HPV22	O13263 xenopus lae
31	43	36.1	152	VNS2_PVM	P28689 pneumonia v
32	43	36.1	296	RIPX_BACSU	P46352 bacillus su
33	43	36.1	334	VE2_BPVA	P08345 bacillus papl

34	43	36.1	375	VE2_HPV26	P36788 human papil
35	43	36.1	431	VE2_HPV23	P50769 human papil
36	43	36.1	1301	PRP9_DROME	P35832 dirosophila
37	42.5	35.7	461	YU2_CAEEL	Q19802 caenorhabdi
38	42.5	35.7	1066	Z295_HUMAN	Q9u1j3 homo sapien
39	42	35.3	282	Y32K_BNYVG	P19313 beet necrot
40	42	35.3	360	VE2_HPV70	P50773 human papil
41	42	35.3	416	RHIC_GORGO	Q28426 gorilla gor
42	42	35.3	499	TMQA_PSEME	O00456 pseudomonas
43	41.5	34.9	2731	RREP_CVMUT	P29982 murine coro
44	41	34.5	199	YB5_MYCPN	P73318 mycoplasma
45	41	34.5	225	UNG_BACSU	P39615 bacillus su

ALIGNMENTS

```

RESULT 1
VE2_HPV16
ID VE2_HPV16 STANDARD: PRT: 365 AA.
AC P03120;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE Regulatory protein E2.
GN E2.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220: PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Roweckamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP FUNCTION.
RX MEDLINE=87198893: PubMed=3033289;
RA Phelps W.C., Howley P.M.;
RT "Transcriptional trans-activation by the human papillomavirus type 16
RT E2 gene product.";
J. Virol. 61:1630-1638(1987).
CC -!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACGNNNNNGGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDENT OF E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC -!- SUBUNIT: BINDS DNA AS A DIMER.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: HPV16, IN COMPARISON TO HPV TYPES 6 AND 11, IS MORE
CC OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.
CC -----
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CC -----
CC EMBL, K02718; AAA46941.1; -.
CC PIR, A03669; W2WLSH.
CC HSSP: P17383; IDHM.
CC Interpro: IPR000427; E2_C.
CC Interpro: IPR001866; E2_N.
CC Pfam: PF00508; E2_N; 1.
CC Pfam: PF00511; E2_C; 1.
CC Prodom: PD000672; E2_C; 1.
CC Prodom: PD000678; E2_N; 1.
DR

```

KW Early protein; Transcription regulation; Activator; DNA-binding;
 KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
 SQ SEQUENCE 365 AA; 41825 MW; 27581F82B246E112 CRC64;

Query Match 100.0%; Score 119; DB 1; Length 365;

Best Local Similarity 100.0%; Pred. No. 9.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 D1CNTMTMTMTHTIYICEE 19
 Db 124 D1CNTMTMTMTHTIYICEE 142

RESULT 2

VE2_HPV35
 ID VE2_HPV35 STANDARD; PRT; 367 AA.
 AC P27222;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Regulatory protein E2.
 GN E2.
 OS Human papillomavirus type 35.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_Taxid=10587;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92124753; PubMed=1310198;
 RA March J.E., Ponsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
 RT "The phylogenetic relationship and complete nucleotide sequence of
 human papillomavirus type 35.";
 RL Virology 186:770-776(1992).
 CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
 IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNGGT-3') PRESENT
 IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
 ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
 WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
 BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
 INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
 REPLICATION.
 CC -1- SUBUNIT: BINDS DNA AS A DIMER.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
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 CC EMBL: X74477; CAAS2564.1; ALT_TERM.
 DR EMBL: M74117; W2WL35.
 DR PIR: S36524; S36524.
 DR HSP: P17383; 1DHM.
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00508; E2_N; 1.
 DR Pfam: PF00511; E2_C; 1.
 DR ProDom: PD000672; E2_C; 1.
 DR ProDom: PD000678; E2_N; 1.
 DR Early protein; Transcription regulation; Activator; DNA-binding;
 KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
 FT CONFLICT 92 92 T -> D (IN REF. 2).
 FT CONFLICT 108 109 OG -> TR (IN REF. 2).

FT CONFLICT 111 111 F -> L (IN REF. 2).
 FT CONFLICT 114 116 HGV -> D (IN REF. 2).
 FT CONFLICT 120 120 V -> A (IN REF. 2).
 FT CONFLICT 303 303 L -> S (IN REF. 2).
 SQ SEQUENCE 367 AA; 41897 MW; 747C197E02C0AF35 CRC64;

Query Match 73.1%; Score 87; DB 1; Length 367;
 Best Local Similarity 87.5%; Pred. No. 2.9e-05;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 NTMTMTMTHTIYICEE 19
 Db 128 NTMTMTMTHTIYILED 143

RESULT 3

VE2_HPV31
 ID VE2_HPV31 STANDARD; PRT; 372 AA.
 AC P17383;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Regulatory protein E2.
 GN E2.
 OS Human papillomavirus type 31.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_Taxid=10585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89299478; PubMed=2545036;
 RA Goldsborough M.D., Dislvestre D., Temple G.F., Lorincz A.T.;
 RT "Nucleotide sequence of human papillomavirus type 31: a cervical
 neoplasia-associated virus.";
 RL Virology 171:306-311(1989).
 [2]
 RP STRUCTURE BY NMR OF 291-372.
 RX MEDLINE-96194130; PubMed=8652551;
 RA Liang H., Petros A.M., Meadows R.P., Yoon H.S., Egan D.A., Walter K.,
 RT Holman T.F., Robins T., Pesik S.W.;
 RT "Solution structure of the DNA-binding domain of a human
 papillomavirus E2 protein: evidence for flexible DNA-binding
 regions.";
 RL Biochemistry 35:2095-2103(1996).
 CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
 IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNGGT-3') PRESENT
 IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
 ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
 WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
 BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
 INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
 REPLICATION.
 CC -1- SUBUNIT: BINDS DNA AS A DIMER.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
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 or send an email to license@sib-sib.ch).
 CC EMBL: J04353; AAA46953.1; -.
 DR PIR: D32444; W2WL31.
 DR PDB: 1DHM; 07-DEC-96.
 DR InterPro: IPR000427; E2_C.
 DR InterPro: IPR001866; E2_N.
 DR Pfam: PF00508; E2_N; 1.
 DR Pfam: PF00511; E2_C; 1.
 DR ProDom: PD000672; E2_C; 1.
 DR ProDom: PD000678; E2_N; 1.
 DR Early protein; Transcription regulation; Activator; DNA-binding;
 KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
 FT CONFLICT 92 92 T -> D (IN REF. 2).
 FT CONFLICT 108 109 OG -> TR (IN REF. 2).

KW Trans-acting factor; DNA replication; Repressor; Nuclear protein;
3D-structure.
SQ SEQUENCE 372 AA; 42104 MW; 4F387C5E3AFB9D1D CRC64;

Query Match 66.4%; Score 79; DB 1; Length 372;
Best Local Similarity 70.6%; Pred. No. 0.0038;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DICTNHTNTHIYICEE 17
1: ||||| |||||
DB 124 DVHNTNHTNMKEIYIC 140

RESULT 4
VE2_HPV58 STANDARD; PRT; 358 AA.

AC P26546;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.

OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10598;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE-92024102; PubMed-1656594;
RA Kiril' Y., Iwamoto S., Matsukura T.;
RL "Human papillomavirus type 58 DNA sequence.";
Virology 185:424-427(1991).

-1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNGGT-3') PRESENT
IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
REPLICATION.

-1- SUBUNIT: BINDS DNA AS A DIMER.
-1- SUBCELLULAR LOCATION: Nuclear.

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DR EMBL: D90400; BAA31848.1;
DR PIR: B36779; W2ML58.
DR HSSP: P17383; IDHM.
DR InterPro: IPR000427; E2_C.
DR InterPro: IPR001866; E2_N.
DR Pfam: PF00508; E2_N; 1.
DR Pfam: PF00511; E2_C; 1.
DR ProDom: PD000672; E2_C; 1.
DR ProDom: PD000678; E2_N; 1.
KW Early protein; Transcription regulation; Activator; DNA-binding;
KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ SEQUENCE 358 AA; 40781 MW; A3CA0BE001E2DIE CRC64;

Query Match 60.5%; Score 72; DB 1; Length 358;
Best Local Similarity 68.4%; Pred. No. 0.0035;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 DICTNHTNTHIYICEE 19
1: ||||| |||||
DB 124 DKANTMDYTNMSEIYIIEE 142

RESULT 5
VE2_HPV33 STANDARD; PRT; 353 AA.

AC P06423;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.

OS Human papillomavirus type 33.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10586;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE-86200464; PubMed-3009902;
RA Cole S.T., Strecek R.E.;
RL "Genome organization and nucleotide sequence of human papillomavirus
type 33, which is associated with cervical cancer.";
J. Virol. 58:991-995(1986).

-1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNGGT-3') PRESENT
IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
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WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
REPLICATION.

-1- SUBUNIT: BINDS DNA AS A DIMER.
-1- SUBCELLULAR LOCATION: Nuclear.

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DR EMBL: M12732; AAA46961.1;
DR PIR: A03670; W2ML33.
DR HSSP: P17383; IDHM.
DR InterPro: IPR000427; E2_C.
DR InterPro: IPR001866; E2_N.
DR Pfam: PF00508; E2_N; 1.
DR Pfam: PF00511; E2_C; 1.
DR ProDom: PD000672; E2_C; 1.
DR ProDom: PD000678; E2_N; 1.
KW Early protein; Transcription regulation; Activator; DNA-binding;
KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ SEQUENCE 353 AA; 40253 MW; 673A9D765DBB1BC CRC64;

Query Match 55.5%; Score 66; DB 1; Length 353;
Best Local Similarity 75.0%; Pred. No. 0.024;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 NTMHTNTHIYICEE 19
1: ||||| |||||
DB 127 NTMDYTNMGEIYIIEE 142

RESULT 6
VE2_PCPIV STANDARD; PRT; 377 AA.

AC O02264;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.

OS Pygmy chimpanzee papillomavirus type 1.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.

```

OX NCBI_TaxID=10576;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92391075; PubMed=1325697;
RA van Ransst M., Fuse A., Fiten P., Beuken E., Pfister H., Burk R.D.,
RT Opendakker G.;
"Human papillomavirus type 13 and pygmy chimpanzee papillomavirus
type 1: comparison of the genome organizations.";
RL Virology 190:587-596(1992).
CC -I- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCCNNNNNGGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC -I- SUBUNIT: BINDS DNA AS A DIMER.
CC -I- SUBCELLULAR LOCATION: Nuclear.
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CC -----
CC EMBL: X62844; CAA44658.1;
CC PIR: D36818; W2WLC1.
CC DR HSSP: P17383; IDHM.
CC DR InterPro: IPR000427; E2_C.
CC DR InterPro: IPR001866; E2_N.
CC DR Pfam: PF00508; E2_N; 1.
CC DR Pfam: PF00511; E2_C; 1.
CC DR ProDom: PD000672; E2_C; 1.
CC DR ProDom: PD000678; E2_N; 1.
CC DR Early protein: Transcription regulation; Activator; DNA-binding;
CC Trans-acting factor; DNA replication; Repressor; Nuclear protein.
CC KW SEQUENCE 377 AA; 43264 MW; B04A6A0DB47FF2CA CRC64;
SQ
Query Match 53.8%; Score 64; DB 1; Length 377;
Best Local Similarity 60.0%; Pred. No. 0.049;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 4 NTMHTNMTHTIYI 18
Db 127 NSMHTVLMKTYVCE 141
RESULT 7
VE2_HPVA2 STANDARD; PRT; 398 AA.
AC P27223;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.
GN E2.
OS Human papillomavirus type 42.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92087479; PubMed=1309278;
RA Philipp W., Honore N., Sapp M., Cole S.T., Strecek R.E.;
RT "Human papillomavirus type 42: new sequences, conserved genome
RT organization ";
RL Virology 186:331-334(1992).
CC -I- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCCNNNNNGGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER

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CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC -I- SUBUNIT: BINDS DNA AS A DIMER.
CC -I- SUBCELLULAR LOCATION: Nuclear.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M73236; AAA47044.1; ALT_INIT.
CC PIR: B39451; W2WLA2.
CC DR HSSP: P17383; IDHM.
CC DR InterPro: IPR000427; E2_C.
CC DR InterPro: IPR001866; E2_N.
CC DR Pfam: PF00508; E2_N; 1.
CC DR Pfam: PF00511; E2_C; 1.
CC DR ProDom: PD000672; E2_C; 1.
CC DR ProDom: PD000678; E2_N; 1.
CC DR Early protein: Transcription regulation; Activator; DNA-binding;
CC Trans-acting factor; DNA replication; Repressor; Nuclear protein.
CC KW SEQUENCE 398 AA; 45309 MW; 4D41D7196372808C CRC64;
SQ
Query Match 52.1%; Score 62; DB 1; Length 398;
Best Local Similarity 76.9%; Pred. No. 0.099;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 4 NTMHTNMTHTIYI 16
Db 127 NSMHTVLMKTYIYI 139
RESULT 8
VE2_HPVS2 STANDARD; PRT; 368 AA.
AC P36796;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.
GN E2.
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RT Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -I- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCCNNNNNGGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC -I- SUBUNIT: BINDS DNA AS A DIMER.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
CC DR EMBL; X74481; CAAS258.1; -.
CC DR PIR; S36576; S36576.
CC DR HSSP; P17383; IDHM.
CC DR InterPro; IPR000427; E2_C.
CC DR InterPro; IPR001866; E2_N.
CC DR Pfam; PF00508; E2_N.1.
CC DR Pfam; PF00511; E2_C.1.
CC DR ProDom; PD000672; E2_C.1.
CC DR ProDom; PD000678; E2_N.1.
CC KW Early protein: Transcription regulation; Activator; DNA-binding;
SO Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SO SEQUENCE 368 AA; 41739 MW; 321B423B52F629D3 CRC64;

OY 4 NTMHTNTWTHIYI--CE 18
Db 127 NTMDYTNKREIYLGECE 144
Query Match 49.2%; Score 58.5; DB 1; Length 368;
Best Local Similarity 61.1%; Pred. No. 0.28;
Matches 11; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

RESULT 9
VE2_HPV32 STANDARD; PRT; 394 AA.
AC P36791;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.
EN E2.
OS Human Papillomavirus type 32.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10612;
RN NM_011111;
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IF BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNGGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC CC -1- SUBUNIT: BINDS DNA AS A DIMER.
CC CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
CC DR EMBL; X74475; CAAS2552.1; -.
CC DR PIR; S36512; S36512.
CC DR HSSP; P17383; IDHM.
CC DR InterPro; IPR000427; E2_C.
CC DR InterPro; IPR001866; E2_N.
CC DR Pfam; PF00511; E2_C.1.
CC DR Pfam; PF00511; E2_N.1.
CC DR ProDom; PD000672; E2_C.1.
CC DR ProDom; PD000678; E2_N.1.
CC KW Early protein: Transcription regulation; Activator; DNA-binding;
SO Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SO SEQUENCE 368 AA; 41739 MW; 321B423B52F629D3 CRC64;

```

QY	4	NTMHTYNTWTHIYI	16	48.7%	Score 58;	DB 1;	Length 394;
Db	127	NAMHTYNTWTHIYV	139	69.2%	Pred. NO. 0.36;		
Matches	9;	Conservative	1;	Mismatches	3;	Indels	0;
QY	4	NTMHTYNTWTHIYI	16				
Db	127	NAMHTYNTWTHIYV	139				

Trans-acting factor: DNA replication; Repressor; Nuclear protein.

SEQUENCE 394 AA; 45038 MW; 113C46119C2265E7 CRC64;

Query Match 48.7%; Score 58; DB 1; Length 394;

Best Local Similarity 69.2%; Pred. NO. 0.36;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 10

VE2_HPV40 STANDARD; PRT; 370 AA.

AC P36793;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Regulatory protein E2.

GN E2.

OS Human papillomavirus type 40.

CC Viruses: dsDNA viruses, no RNA stage; Papillomaviridae;

CC Papillomavirus.

CC NCBI_TaxID=10615;

CC [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=94265501; Pubmed=8205838;

RA Dellijs H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types.";

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

CC IF BINDS TO THE E2E RESPONSE ELEMENT (5'-ACNNNNNGT-3') PRESENT

CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER

CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING ON E2E'S POSITION

CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA

CC REPLICATION.

CC -1- SUBUNIT: BINDS DNA AS A DIMER.

CC -1- SUBCELLULAR LOCATION: Nuclear.

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DR EMBL: X74478; CAA52570.1; -

DR PIR: S36558; S36558.

DR HSSP: P17383; IDHM.

DR InterPro: IPR000427; E2_C.

DR InterPro: IPR001866; E2_N.

DR Pfam: PF00508; E2_N.1.

DR Pfam: PF00511; E2_C.1.

DR ProDom: PD000672; E2_C.1.

DR ProDom: PD000678; E2_N.1.

KW Early protein; Transcription regulation; Activator; DNA-binding;

KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.

SQ SEQUENCE 370 AA; 41767 MW; 02C60C5137938F72 CRC64;

Query Match 46.2%; Score 55; DB 1; Length 370;

Best Local Similarity 61.5%; Pred. NO. 0.88;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 NTMHTYNTWTHIYI 16

I I I I I I I I I I

Db 127 NAMHTYNTWTHIYV 139

RESULT 11

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VE2_HPV07          STANDARD;          PRT;          375 AA.
ID   VE2_HPV07
AC   P36779;
DT   01-JUN-1994 (rel. 29, Created)
DT   01-JUN-1994 (rel. 29, Last sequence update)
DT   15-JUL-1998 (rel. 36, Last annotation update)
DE   Regulatory protein E2.
E2.
OS   Human papillomavirus type 7.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX   NCBI_TaxID=10620;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94265501; PubMed=8205838;
RA   Delius H., Hofmann B.;
RT   "Primer-directed sequencing of human papillomavirus types.";
RL   Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC   -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC   IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCCNNNNNGGT-3') PRESENT
CC   IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC   ACTIVATE OR REPRESS TRANSCRIPTION DEPENDENT OF E2RE'S POSITION
CC   WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC   BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC   INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC   REPLICATION.
CC   -1- SUBUNIT: BINDS DNA AS A DIMER.
CC   -1- SUBCELLULAR LOCATION: Nuclear.
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CC   -----
DR   EMBL; X74463; CAA52479.1; -.
DR   PIR; S36587; S36587.
DR   HSSP; P17383; 1DHM.
DR   InterPro: IPR000427; E2_C.
DR   InterPro: IPR001866; E2_N.
DR   Pfam; PF00508; E2_N; 1.
DR   Pfam; PF00511; E2_C; 1.
DR   ProDom; PD000672; E2_C; 1.
DR   ProDom; PD000678; E2_N; 1.
KW   Early protein; Transcription regulation; Activator; DNA-binding;
KW   Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ   SEQUENCE 375 AA; 42695 MW; 367F0363F8E984DA CRC64;

Query Match          46.2%; Score 55; DB 1; Length 375;
Best Local Similarity 61.5%; Pred. No. 0.9;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY   4 NTMHTNMTHIYI 16
    1 1111111111
DB   127 NAMHTYLTAVYV 139

RESULT 12
VE2_HPV13          STANDARD;          PRT;          377 AA.
ID   VE2_HPV13
AC   Q02263;
DT   01-APR-1993 (rel. 25, Created)
DT   01-APR-1993 (rel. 25, Last sequence update)
DT   15-JUL-1998 (rel. 36, Last annotation update)
DE   Regulatory protein E2.
E2.
OS   Human papillomavirus type 13.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX   NCBI_TaxID=10573;
RN   [1]

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RP   SEQUENCE FROM N.A.
RX   MEDLINE=92391075; PubMed=1325697;
RA   van Raest M., Fuse A., Filten P., Beuken E., Pfister H., Burk R.D.,
RA   Opdenakker G.;
RT   "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus
RT   type 1: comparison of the genome organizations.";
RL   Virology 190:587-596(1992).
CC   -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC   IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCCNNNNNGGT-3') PRESENT
CC   IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC   ACTIVATE OR REPRESS TRANSCRIPTION DEPENDENT OF E2RE'S POSITION
CC   WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC   BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC   INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC   REPLICATION.
CC   -1- SUBUNIT: BINDS DNA AS A DIMER.
CC   -1- SUBCELLULAR LOCATION: Nuclear.
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CC   -----
DR   EMBL; X62843; CAA44650.1; -.
DR   PIR; DA2955; W2ML13.
DR   HSSP; P17383; 1DHM.
DR   InterPro: IPR000427; E2_C.
DR   InterPro: IPR001866; E2_N.
DR   Pfam; PF00508; E2_N; 1.
DR   Pfam; PF00511; E2_C; 1.
DR   ProDom; PD000672; E2_C; 1.
DR   ProDom; PD000678; E2_N; 1.
KW   Early protein; Transcription regulation; Activator; DNA-binding;
KW   Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ   SEQUENCE 377 AA; 43101 MW; BE0496B486BC303 CRC64;

Query Match          44.1%; Score 52.5; DB 1; Length 377;
Best Local Similarity 52.9%; Pred. No. 2;
Matches 9; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY   3 CNT--MHTNMTHIYI 16
    111111111111
DB   123 CNTNDMDYVSMYIYV 139

RESULT 13
VE2_HPV11          STANDARD;          PRT;          367 AA.
ID   VE2_HPV11
AC   P04015;
DT   23-OCT-1986 (rel. 02, Created)
DT   23-OCT-1986 (rel. 02, Last sequence update)
DT   15-JUL-1998 (rel. 36, Last annotation update)
DE   Regulatory protein E2.
E2.
OS   Human papillomavirus type 11.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX   NCBI_TaxID=10580;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86181601; PubMed=3008427;
RA   Dartmann K., Schwarz E., Gissmann L., zur Hausen H.;
RT   "The nucleotide sequence and genome organization of human papilloma
RT   virus type 11.";
RL   Virology 151:124-130(1986).
CC   -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC   IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCCNNNNNGGT-3') PRESENT
CC   IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC   ACTIVATE OR REPRESS TRANSCRIPTION DEPENDENT OF E2RE'S POSITION
CC   WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC   -----

```

```

CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC
CC -I- SUBUNIT: BINDS DNA AS A DIMER.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL, M14119; AAA46930.1; -.
CC PIR; A03668; WZWLL1.
CC DR HSSP; P17383; IDHM.
CC DR InterPro; IPR000427; E2_C.
CC DR InterPro; IPR001866; E2_N.
CC Pfam; PF00508; E2_N; 1.
CC DR Pfam; PF00511; E2_C; 1.
CC DR ProDom; PD000672; E2_C; 1.
CC DR ProDom; PD000678; E2_N; 1.
CC KW Early protein: Transcription regulation; Activator; DNA-binding;
CC Trans-acting factor; DNA replication; Repressor; Nuclear protein.
CC SEQUENCE 367 AA; 41709 MW; F7BAF4D358504F0 CRC64;
CC
CC -----
CC Query Match 43.7%; Score 52; DB 1; Length 367;
CC Best Local Similarity 61.5%; Pred. No. 2.3;
CC Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
CC
CC OY 4 NTMTATNTNTHYI 16
CC I I I I I I I I
CC Db 127 NYMEYVWTHYIL 139
CC
CC -----
CC RESULT 14
CC VE2_RHPV1
CC ID_VE2_RHPV1 STANDARD; PRT; 366 AA.
CC
CC AC P23156;
CC DT 01-AUG-1991 (Rel. 19, Created)
CC DT 01-AUG-1991 (Rel. 19, Last sequence update)
CC DT 15-JUL-1998 (Rel. 36, Last annotation update)
CC DE Regulatory protein E2.
CC GN E2.
CC OS Rhesus papillomavirus type 1 (Rhpv 1).
CC OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC OC Papillomavirus.
CC OX NCBI_TaxID=10570;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=91135018; PubMed=1847267;
CC RA Ostrow R.S., Labresh K.V., Fatas A.J.;
CC RT "Characterization of the complete RHPV 1 genomic sequence and an
CC integration locus from a metastatic tumor.";
CC RL Virology 181:424-429(1991).
CC
CC -I- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACGNNNNNGGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDENT OF E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC
CC -I- SUBUNIT: BINDS DNA AS A DIMER.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC
CC -----
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CC      or send an email to license@isb-sib.ch.
CC      -----
CC      EMBL, M60184; AAA79314.1; -.
CC      DR      PIR, D38503; W2WLR1.
CC      DR      HSSP, P17383; IDHM.
CC      DR      InterPro: IPR000427; E2_C.
CC      DR      InterPro: IPR001866; E2_N.
CC      DR      Pfam, PF00508; E2_N; 1.
CC      DR      Pfam, PF00511; E2_C; 1.
CC      DR      Pfam, PF00572; E2_C; 1.
CC      DR      ProDom, PD000678; E2_N; 1.
CC      KW      Early protein: Transcription regulation; Activator; DNA-binding;
CC      KW      Trans-acting factor; DNA replication; Repressor; Nuclear protein.
CC      SO      SEQUENCE 366 AA; 41025 MW; 44A627E20DA12284 CRC64;
CC
CC      Query Match          42.9%; Score 51; DB 1; Length 366;
CC      Best Local Similarity 61.5%; Pred. No. 3.2;
CC      Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
CC
CC      QY      4 NTMHTYNTHTIYI 16
CC              ||| | | |||
CC      DB      128 NTMEYVLWGHTIYV 140
CC
CC      RESULT 15
CC      VE2_HPV60          STANDARD; PRT; 404 AA.
CC      AC      Q80944;
CC      DT      15-JUL-1998 (Rel. 36, Created)
CC      DT      15-JUL-1998 (Rel. 36, Last sequence update)
CC      DE      15-JUL-1998 (Rel. 36, Last annotation update)
CC      DE      Regulatory protein E2.
CC      GN      E2.
CC      OS      Human papillomavirus type 60.
CC      OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC      OC      Papillomavirus.
CC      RN      NCBI_TaxID=40540;
CC      RP      [1]
CC      RA      SEQUENCE FROM N.A.
CC      RA      Delius H.;
CC      RL      Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC      CC      -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC      CC      IT BINDS TO THE E2E RESPONSE ELEMENT (5'-ACNNNNNGGT-3') PRESENT
CC      CC      IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC      CC      ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2E'S POSITION
CC      CC      BY REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC      CC      BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC      CC      INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC      CC      REPLICATION.
CC      CC      -1- SUBUNIT: BINDS DNA AS A DIMER.
CC      CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      CC      -----
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      CC      use by non-profit institutions as long as its content is in no way
CC      CC      modified and this statement is not removed. Usage by and for commercial
CC      CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      CC      or send an email to license@isb-sib.ch).
CC      CC      -----
CC      CC      EMBL, U31792; AAA79488.1; -.
CC      DR      HSSP, P03122; 2BOP.
CC      DR      InterPro: IPR000427; E2_C.
CC      DR      InterPro: IPR001866; E2_N.
CC      DR      Pfam, PF00508; E2_N; 1.
CC      DR      Pfam, PF00511; E2_C; 1.
CC      DR      ProDom, PD000678; E2_C; 1.
CC      DR      ProDom, PD000678; E2_N; 1.
CC      KW      Early protein: Transcription regulation; Activator; DNA-binding;
CC      KW      Trans-acting factor; DNA replication; Repressor; Nuclear protein.
CC      SO      SEQUENCE 404 AA; 46534 MW; 73B8CA8508720D00 CRC64;
CC

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Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 NTMHTNTHTIY 15
|| |||| :||
DB 129 NTPPTNMEIY 140

Search completed: January 14, 2003, 18:40:11
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:37:13 : Search time 36 Seconds
(without alignments)
70.327 Million cell updates/sec

Title: US-09-828-645-1

Perfect score: 119
Sequence: 1 DIGNTHMYNTMTHTYICEE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

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20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	19	AAU10801	Human papillomavir
2	119	100.0	20	AAU15550	Immunopeptide #1 d
3	119	100.0	147	AAE15402	HPV 16 E2 protein
4	119	100.0	201	AAW74333	Human papillomavir
5	119	100.0	365	AAW12095	Human papillomavir
6	119	100.0	365	AAW50005	Human papillomavir
7	119	100.0	365	AAW50005	Human papillomavir
8	119	100.0	365	AAW50005	Human papillomavir
9	119	100.0	365	AAW50005	Human papillomavir
10	119	100.0	365	AAW50005	Human papillomavir

11	109	91.6	20	AAU15553	Immunopeptide #4 d
12	97	81.5	19	AAU10806	Human papillomavir
13	79	66.4	20	AAU15591	Immunopeptide #1 d
14	79	66.4	372	AAU98432	Human papillomavir
15	66	55.5	353	AAU98445	Human papillomavir
16	57	47.9	20	AAU15596	Immunopeptide deri
17	52	43.7	148	AAU15535	Immunopeptide deri
18	52	43.7	201	AAU74335	HPV 11 E2 protein.
19	52	43.7	315	AAU18268	Human papillomavir
20	52	43.7	315	AAU18272	Human G-protein co
21	52	43.7	315	AAU18273	Human G-protein co
22	52	43.7	315	AAU18274	Human G-protein co
23	52	43.7	315	AAU18275	Human G-protein co
24	52	43.7	315	AAU18276	Human G-protein co
25	52	43.7	315	AAU18277	Human G-protein co
26	52	43.7	315	AAU18278	Human G-protein co
27	52	43.7	315	AAU18279	Human G-protein co
28	52	43.7	315	AAU18280	Human G-protein co
29	52	43.7	317	AAU95677	Human G-protein an
30	52	43.7	334	AAU24698	Human olfactory re
31	52	43.7	334	AAU71887	Human olfactory re
32	52	43.7	334	AAU67468	Breast amplified G
33	52	43.7	334	AAU67468	Breast amplified G
34	52	43.7	334	AAU67468	Breast amplified G
35	52	43.7	334	AAU67468	Breast amplified G
36	52	43.7	334	AAU67468	Breast amplified G
37	52	43.7	334	AAU67468	Breast amplified G
38	52	43.7	334	AAU67468	Breast amplified G
39	52	43.7	334	AAU67468	Breast amplified G
40	52	43.7	334	AAU67468	Breast amplified G
41	52	43.7	334	AAU67468	Breast amplified G
42	52	43.7	334	AAU67468	Breast amplified G
43	50	42.0	363	AAU78368	Human protein SEQ
44	50	42.0	436	AAU78368	Human prostate can
45	50	42.0	436	AAU78368	Human prostate can

ALIGNMENTS

RESULT 1

AAU10801

ID AAU10801 standard; peptide: 19 AA.

AC AAU10801:

DT 14-FEB-2002 (first entry)

XX

DE Human papillomavirus (HPV) 16 E2 coding region derived peptide #1.

XX

KW Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma;

KW adenocarcinoma; kolloidosis; hyperkeratosis; intraepithelial neoplasia;

KW intraepithelial lesion; dysplasia; head cancer; neck cancer;

KW small cell lung cancer; melanoma; oncogene.

OS Human papillomavirus 16.

XX

PN MO200177142-A1.

PD 18-OCT-2001.

XX

PF 05-APR-2001; 2001MO-US11233.

XX

PR 05-APR-2000; 2000US-194796P.

XX

PA (IMPA-) IMPACT DIAGNOSTICS INC.

XX

PI Hu YX;

XX

DR WPI; 2002-010888/01.

XX

PT New peptides derived from E2, E6 or E7 early coding regions of human papillomavirus 16 and 18, useful in diagnosis of human papillomavirus

PT Infection and associated malignancy e.g. cervical carcinoma
 XX
 PS Claim 2; Fig 2; 28pp; English.
 XX
 CC The invention describes a novel peptide derived from the E2, E6 or E7
 CC early coding region of human papillomavirus (HPV) 16 and 18, which is
 CC soluble in aqueous solution and has a lysine or cysteine residue near the
 CC amino terminus, very few tryptophan, methionine and cysteine residues,
 CC and/or many glycine and asparagine residues. The peptides and diagnostic
 CC method are used to diagnose HPV infection, especially infection with
 CC oncogenic HPV by using peptides derived from the E2 region, since HPV 16
 CC and 18 are the main HPV genetic types associated with cancers, and
 CC presence of antibodies to E2 protein is known to provide evidence of HPV
 CC infection. They are also useful to diagnose HPV associated malignancy or
 CC premalignancy, especially carcinoma by using peptides derived from the E6
 CC or E7 regions, since E6 and E7 are thought to be tumour-specific
 CC antigens. The peptides and diagnostic method are especially useful to
 CC diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix)
 CC and any HPV associated epithelial cell abnormality including high grade
 CC dysplasias, koilocytosis, hyperkeratosis, precancerous conditions
 CC encompassing intraepithelial neoplasias or intraepithelial lesions, and
 CC invasive or malignant cancers. They are also used to detect head and neck
 CC cancers, small cell lung cancers, penal and anal squamous cell carcinomas
 CC and melanoma. This is the amino acid sequence of peptide epitope #1,
 CC derived from the E2 early coding region of HPV 16, an oncoprotein
 CC involved in the integration of the viral genome into the host cell genome
 CC by the HPV types associated with malignant cancers, described in the
 CC method of the invention.
 CC
 SQ Sequence 19 AA;
 QY Query Match 100.0%; Score 119; DB 23; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 DICTMHTMTWTHYICEE 19
 1 DICTMHTMTWTHYICEE 19
 DB 1 DICTMHTMTWTHYICEE 19

RESULT 2
 AAR15550
 ID AAR15550 standard; Protein; 20 AA.
 XX
 AC AAR15550;
 XX
 DT 02-MAR-1992 (first entry)
 XX
 DE Immunoepitope #1 derived from HPV16 E2 peptide.
 XX
 KW cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
 KW squamous cell carcinoma; ELISA; HPV 16.
 XX
 OS Synthetic.
 XX
 PN WO9118294-A.
 PD 28-NOV-1991.
 XX
 PF 13-MAY-1991; 91WO-SF00335.
 XX
 PR 11-MAY-1990; 90SE-0001705.
 XX
 PA (MEDS-) MEDSCAND AB.
 XX
 PI Dillner J, Dillner L, Cheng HK;
 DR WPI; 1991-369390/50.
 XX
 PT Diagnosis of human papilloma virus infection and PV-carrying
 PT tumours - using synthetic peptide(s) to detect virus specific
 PT antigen-antibody complexes by Immunoassay
 XX

PS Disclosure; Page 38; 72pp; English.
 XX
 CC This is one of a large number of peptides which have been
 CC synthesised on the basis of the amino acid sequences for the E2, E4,
 CC E7, L1 or L2 proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The
 CC selection of peptide sequences was based on the assumption that an
 CC immunoreactive region might be situated in the same relative region
 CC of a protein from different HPV types. The peptides were used in
 CC diagnostic immunoassays to detect HPV-infection.
 CC See AAR15523-R15601.
 XX
 SQ Sequence 20 AA;
 QY Query Match 100.0%; Score 119; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 DICTMHTMTWTHYICEE 19
 2 DICTMHTMTWTHYICEE 20
 DB 2 DICTMHTMTWTHYICEE 20

RESULT 3
 AAE15402
 ID AAE15402 standard; Protein; 147 AA.
 XX
 AC AAE15402;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE HPV 16 E2 protein.
 XX
 KW Human papillomavirus; HPV 16 E2 protein; cytotoxic gene; anogenital SCC;
 KW cancer; intraepithelial neoplasia; IN; squamous cell carcinoma;
 KW tumour; gene therapy; keratinocyte.
 XX
 OS Human papillomavirus.
 XX
 PN WO200187350-A2.
 PD 22-NOV-2001.
 XX
 PF 11-MAY-2001; 2001WO-US15407.
 XX
 PR 12-MAY-2000; 2000US-203709P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Sethl N, Palefsky J;
 DR WPI; 2002-082947/11.
 XX
 PT Novel gene therapy approach to specifically eliminate keratinocytes or
 PT other cells expressing human papilloma virus, involves transfecting
 PT cell with a construct encoding HPV specific promoter induced by a HPV
 PT protein
 XX
 PS Example 1; Fig 13; 72pp; English.
 XX
 CC The invention provides a novel gene therapy approach to specifically
 CC eliminate keratinocytes or other cells expressing early
 CC human papillomavirus (HPV) and which is minimally toxic to HPV-negative
 CC cells. The method involves transfecting a mammalian cell with a
 CC nucleic acid construct encoding a HPV specific promoter that is induced
 CC by a HPV protein where the promoter is operably linked to a nucleic
 CC acid comprising a cytotoxic gene such that the cell, when infected with
 CC a HPV, induces expression of the cytotoxic gene resulting in death of
 CC the mammalian cell. The method is useful for selectively killing a
 CC cancer cell comprising intraepithelial neoplasia (IN), anogenital
 CC cancer or a metastatic cell or solid tumour bearing a HPV. The nucleic
 CC acid construct comprising HPV promoter operably linked to a reporter
 CC gene is useful for selectively labelling a cell bearing HPV. The method
 CC is useful for specifically eliminating keratinocytes, particularly cells

CC of anogenital squamous cell carcinoma (SCC), or other cells expressing
 CC early HPV e-9. HPV 16 genes and a cell comprising a wart. The present
 CC sequence is HPV 16 E2 protein.

SO Sequence 147 AA:

Query Match 100.0%; Score 119; DB 23; Length 147;
 Best Local Similarity 100.0%; Pred. No. 9.9e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTMHYTNWTHIYCEE 19
 DB 60 DICTMHYTNWTHIYCEE 78

RESULT 4

ID AAB74333 standard; Protein; 201 AA.

AC AAB74333;

DT 29-JUN-2001 (first entry)

DE Human papillomavirus 16 E2NT module.

KM E2NT; antiviral; warts; proliferative skin lesion; cervical cancer;

KW HPV.

OS Human papillomavirus.

PN WO200121645-A2.

PD 29-MAR-2001.

PF 18-SEP-2000; 2000WO-GB03568.

PR 17-SEP-1999; 99GB-0021938.

PA (UYVO-) UNIV YORK.

PI Antison A, Maitland N;

DR WPI; 2001-328091/34.

PT Crystallized molecular complex of the nuclear phosphoprotein E2

PT N-terminal module useful in drug design for the treatment of conditions

PS associated with human papilloma virus infection

PS Disclosure: Fig 1; 87pp; English.

CC The present invention relates to a crystallized molecular complex
 CC of an E2 N-terminal module (E2NT) dimer protein or its homologue having
 CC residues vital for transcription and replication activities of the
 CC protein. The invention is used to identify antiviral agents, and to
 CC prepare treatments for conditions that arise from herpes papillomavirus
 CC infection, particularly warts, proliferative skin lesions and/or
 CC cervical cancer. The present sequence is the E2NT module of HPV16.

SO Sequence 201 AA:

Query Match 100.0%; Score 119; DB 22; Length 201;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTMHYTNWTHIYCEE 19
 DB 124 DICTMHYTNWTHIYCEE 142

RESULT 5

ID AAM12095 standard; Protein; 365 AA.

XX

AC AAM12095;

DT 28-APR-1997 (first entry)

DE Human papillomavirus-16 E2 protein.

KM Papillomavirus E1/E2 interaction domain; cancer; diagnosis; BPV-1;

KW HPV-16; E2 protein.

OS Human papillomavirus type 16.

FN key Location/Qualifiers

FT Domain

FT 1..190

FT /label= "E1/E2 interaction domain preferred for use

PN WO9641018-A1.

PD 19-DEC-1996.

PF 24-MAY-1996; 96WO-US07615.

PR 07-JUN-1995; 95US-0472666.

PA (HARD) HARVARD COLLEGE.

PI Benson JD, Howley PM, Sakai H, Yasugi T;

DR WPI; 1997-077280/07.

PT Determining pathogenic state of papilloma virus (PV) infected cell -
 PT by testing ability to bind PV E1/E2 interaction domain, failure to
 PT bind indicating a (pre)cancerous condition

PS Claim 2; Page 54-55; 72pp; English.

CC The human papillomavirus (HPV) E2 protein (AAM12095) contains an
 CC E1/E2 interaction domain that specifically reacts with the HPV E1
 CC protein (AAM12094). The interaction domain was identified using a
 CC yeast interaction trap system with E1 fragments as bait and E2
 CC fragments as prey. Bovine papillomavirus (BPV) E1/E2 interaction
 CC domains have also been identified (see AAM12092-93). HPV and BPV
 CC E1/E2 interaction domains can be used to determine the pathogenic
 CC status of a cell; non-cancerous PV-infected cells will bind the
 CC interaction domain, but (pre)cancerous cells will not. The
 CC interaction domains can also be used in methods for typing HPV
 CC infections, inhibiting PV replication, and identifying inhibitors
 CC of PV replication.

SO Sequence 365 AA:

Query Match 100.0%; Score 119; DB 18; Length 365;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTMHYTNWTHIYCEE 19
 DB 124 DICTMHYTNWTHIYCEE 142

RESULT 6

ID AAM50005 standard; Protein; 365 AA.

AC AAM50005;

DT 11-JUN-1998 (first entry)

DE Human papillomavirus-16 E2 protein.

KW Human papillomavirus-16; HPV-16; E2 protein; infection; treatment;
 KW wart; epidermodysplasia verruciformis; laryngeal papilloma;

KW cervical carcinoma.
XX
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT 1..198
FT /note="Transcription activating domain"
FT 281..365
FT /note="DNA-binding domain"
XX
PN MO9801148-A1.
XX
PD 15-JAN-1998.
XX
PF 08-JUL-1997; 97MO-US11815.
XX
PR 09-JUL-1996; 96US-0677206.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Dowhanick JJ, Howley PM;
XX
DR WPI; 1998-100815/09.
XX
DR N-PSDB; AAV18817.
XX
PT Treating papilloma virus infections, by repressing E6 and E7
PT oncogenic proteins - using E2 polypeptide or nucleic acid encoding
PT it, useful for treating warts and cervical cancer
XX
PS Claim 22: Pages 48-49; 71pp; English.
XX
CC The present sequence is the human papillomavirus-16 (HPV-16)
CC E2 protein.
CC Papillomavirus infections can be treated by administering an E2
CC protein, comprising a DNA-binding and transcription activating
CC domain, or the gene encoding the E2 protein to infected cells. The
CC method is applicable to livestock, zoo animals, pets and humans,
CC specifically for the treatment, prevention or reversal of warts,
CC e.g. plantar, common, Butcher's common, flat or genital warts, or
CC epidermodysplasia verruciformis, or growth of papillomavirus
CC transformed cells, especially laryngeal papilloma or cervical
CC carcinoma.
XX
SQ Sequence 365 AA;
XX
Query Match 100.0%; Score 119; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DICTMHTMTHTHYICEE 19
DB 124 DICTMHTMTHTHYICEE 142
RESULT 7
AAB98418
ID AAB98418 standard; Protein; 365 AA.
XX
AC AAB98418;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human papillomavirus protein HPV16 E2.
XX
KW Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW HPV; epitope; T cell; identification; vaccine; infection; genital wart;
KW neoplastic growth; antiviral.
XX
OS Human papillomavirus.
XX
PN WO200141799-A1.
XX
PD 14-JUN-2001.

XX
PF 11-DEC-2000; 2000MO-US33549.
XX
PR 10-DEC-1999; 99US-0172705.
XX
PR 15-AUG-2000; 2000US-0641528.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Settle A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HW;
XX
DR WPI; 2001-381497/40.
XX
PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections -
XX
PS Disclosure; Page 20; 756pp; English.
XX
CC The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (1) has antiviral activity, and can be used in
CC vaccine production. Peptides and corresponding nucleic acid compositions
CC from the present invention are useful for stimulating an immune response
CC to HPV by stimulating the production of CTL or HTL responses,
CC specifically in the treatment or prophylaxis of HPV infection, in persons
CC who have not manifested symptoms e.g. genital warts or neoplastic growth.
CC The peptides can also be used in a tetramer staining assay to assess
CC peripheral blood mononuclear cells for the presence of antigen-specific
CC CTLs following exposure to a pathogen or immunogen, and as reagents to
CC evaluate immune recall responses or evaluate the efficacy of a vaccine.
CC The vaccine compositions are useful for removing warts or treating HPV
CC infections. The epitopes for inclusion in an epitope-base vaccine may
CC be selected from conserved regions of viral or tumour-associated
CC antigens, which reduces the likelihood of escape mutants, also
CC immunosuppressive epitopes that may be present in whole antigens can be
CC avoided with the use of epitope-base vaccines. An additional advantage
CC is the ability to combine selected epitopes (CTL and HTL) and to modify
CC the composition of the epitopes achieving enhanced immunogenicity, the
CC major benefit of the vaccine is that is safe and efficacious. AAB98391
CC to AAB98477 represent polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 365 AA;
XX
Query Match 100.0%; Score 119; DB 22; Length 365;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DICTMHTMTHTHYICEE 19
DB 124 DICTMHTMTHTHYICEE 142
RESULT 8
AAB35191
ID AAB35191 standard; Protein; 365 AA.
XX
AC AAB35191;
XX
DT 24-APR-2001 (first entry)
XX
DE Human papillomavirus HPV16 E2 protein.
XX
KW Papillomavirus; apoptosis; cell death induction; E2 protein; E7 protein;
KW p53; cancer.
XX
OS Human papillomavirus.
XX
PN WO200103717-A2.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000MO-GB02693.
XX
PR 13-JUL-1999; 99GB-0016363.

```

XX (UYBR-) UNIV BRISTOL.
PA
XX
XX Gaston KL, Stern PL, Clarke AR;
XX
XX WPI: 2001-123139/13.
DR
XX N-PSDB: AAF24352.
XX
PT Inducing cell death in papillomavirus (PV) positive or negative
PT oncogenic cells, wild-type, p53 mutant- or p53 related gene positive
PT cells using PV E2 and/or E7 protein or its functional portion or
PT derivative -
XX
PS Disclosure: Fig 9; 55pp; English.
XX
XX The present invention describes a method of inducing apoptotic cell death
CC in papillomavirus negative and positive cells using the papillomavirus
CC E2 and E7 proteins. This can be used in the treatment of epithelial cell
CC cancers, including cervical cancer. The present sequence is the HPV16
CC E2 protein.
XX
XX Sequence 365 AA:
SQ
XX
XX Query Match 100.0%; Score 119; DB 22; Length 365;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-09;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 D1CNTMHTNTMTHIYCEE 19
DB 124 D1CNTMHTNTMTHIYCEE 142
IIIIIIIIIIIIIIIIIIII
RESULT 9
AAB35192
ID AAB35192 standard; Protein; 365 AA.
XX
XX AAB35192;
AC
XX
XX 24-APR-2001 (first entry)
DT
XX
XX Human papillomavirus HPV16 E2DBM protein.
DE
XX
XX Papillomavirus; apoptosis; cell death induction; E2 protein; E7 protein;
KW p53; cancer.
XX
XX Human papillomavirus.
OS
XX
XX WO200103717-A2.
PN
XX
XX 18-JAN-2001.
PD
XX
XX 13-JUL-2000; 2000WO-GB02693.
PF
XX
XX 13-JUL-1999; 99GB-0016363.
PR
XX
XX (UYBR-) UNIV BRISTOL.
PA
XX
XX Gaston KL, Stern PL, Clarke AR;
PI
XX
XX WPI: 2001-123139/13.
DR
XX
XX N-PSDB: AAF24353.
XX
XX Inducing cell death in papillomavirus (PV) positive or negative
PT oncogenic cells, wild-type, p53 mutant- or p53 related gene positive
PT cells using PV E2 and/or E7 protein or its functional portion or
PT derivative -
XX
XX Disclosure: Fig 10; 55pp; English.
XX
XX The present invention describes a method of inducing apoptotic cell death
CC in papillomavirus negative and positive cells using the papillomavirus
CC E2 and E7 proteins. This can be used in the treatment of epithelial cell
CC cancers, including cervical cancer. The present sequence is the HPV16

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CC E2DBM protein.
XX
XX Sequence 365 AA:
SQ
XX
XX Query Match 100.0%; Score 119; DB 22; Length 365;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-09;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 D1CNTMHTNTMTHIYCEE 19
DB 124 D1CNTMHTNTMTHIYCEE 142
IIIIIIIIIIIIIIIIIIII
RESULT 10
AAU10809
ID AAU10809 standard; Protein; 365 AA.
XX
XX AAU10809;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Human papillomavirus (HPV) 16, E2 coding region.
XX
XX Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma;
DE adenocarcinoma; koiocytosis; hyperkeratosis; intraepithelial neoplasia;
KW intraepithelial lesion; dysplasia; head cancer; neck cancer;
KW small cell lung cancer; melanoma; oncogene.
XX
XX Human papillomavirus 16.
OS
XX
XX Key Location/Qualifiers
XX Peptide 124..142
XX FT /label= "E2.peptide_epitope_1
XX FT /note= "This region is specifically referred to
XX FT in claim 2"
XX FT Peptide 328..343
XX FT /label= "E2.peptide_epitope_2
XX FT /note= "This region is specifically referred to
XX FT in claim 2"
XX
XX WO200177142-A1.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 05-APR-2001; 2001WO-US11233.
PF
XX
XX 05-APR-2000; 2000US-194796P.
PR
XX
XX (IMPA-) IMPACT DIAGNOSTICS INC.
PA
XX
XX Hu YX;
PI
XX
XX WPI: 2002-010888/01.
DR
XX
XX New peptides derived from E2, E6 or E7 early coding regions of human
XX papillomavirus 16 and 18, useful in diagnosis of human papillomavirus
XX infection and associated malignancy e.g. cervical carcinoma
XX
XX Disclosure: Fig 2; 28pp; English.
XX
XX The invention describes a novel peptide derived from the E2, E6 or E7
XX early coding region of human papillomavirus (HPV) 16 and 18, which is
XX soluble in aqueous solution and has a lysine or cysteine residue near the
XX amino terminus, very few tryptophan, methionine and cysteine residues,
XX and/or many glycine and asparagine residues. The peptides and diagnostic
XX method are used to diagnose HPV infection, especially infection with
XX oncogenic HPV by using peptides derived from the E2 region, since HPV 16
XX and 18 are the main HPV genetic types associated with cancers, and
XX presence of antibodies to E2 protein is known to provide evidence of HPV
XX infection. They are also useful to diagnose HPV associated malignancy or
XX premalignancy, especially carcinoma by using peptides derived from the E6
XX or E7 regions, since E6 and E7 are thought to be tumour-specific
XX antigens. The peptides and diagnostic method are especially useful to

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CC diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix)
 CC and any HPV associated epithelial cell abnormality including high grade
 CC dysplasias, koilocytosis, hyperkeratosis, precancerous conditions
 CC encompassing intraepithelial neoplasias or intraepithelial lesions, and
 CC invasive or malignant cancers. They are also used to detect head and neck
 CC cancers, small cell lung cancers, penial and anal squamous cell carcinomas
 CC and melanoma. This is the amino acid sequence of the E2 early coding
 CC region of HPV 16, an oncoprotein involved in the integration of the viral
 CC genome into the host cell genome by the HPV types associated with
 CC malignant cancers, described in the method of the invention.

XX Sequence 365 AA;

Query Match 100.0%; Score 119; DB 23; Length 365;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTNTHYNTMTHIYIC 19

DB 124 DICTNTHYNTMTHIYIC 142

RESULT 11

AAR1553 standard; Protein; 20 AA.

AC AAR1553;

DT 02-MAR-1992 (first entry)

DE Immunopeptide #4 derived from HPV16 E2 peptide.

KM cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
 KM squamous cell carcinoma; ELISA; HPV 16.

OS Synthetic.

PN WO9118294-A.

PD 28-NOV-1991.

PF 13-MAY-1991; 91WO-SE00335.

PR 11-MAY-1990; 90SE-0001705.

PA (MEDS-) MEDSCAND AB.

PI Dillner J, Dillner L, Cheng HM;

DR WPI; 1991-369390/50.

PT Diagnosis of human papilloma virus infection and PV-carrying
 PT tumors - using synthetic peptide(s) to detect virus specific
 PT antigen-antibody complexes by immunoassay

PS Disclosure: Page 38; 72pp; English.

XX This is one of a large number of peptides which have been
 CC synthesised on the basis of the amino acid sequences for the E2, E4,
 CC E7, L1 or L2 proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The
 CC selection of peptide sequences was based on the assumption that an
 CC immunoreactive region might be situated in the same relative region
 CC of a protein from different HPV types. The peptides were used in
 CC diagnostic immunoassays to detect HPV-infection.
 CC See AAR1553-R15601.

XX Sequence 20 AA;

Query Match 91.6%; Score 109; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DICTNTHYNTMTHIYIC 17

DB 4 DICTNTHYNTMTHIYIC 20

RESULT 12

AAU10806 standard; peptide; 19 AA.

AC AAU10806;

DT 14-FEB-2002 (first entry)

DE Human papillomavirus (HPV) 16 E2 coding region derived peptide #3.

KM Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma;
 KM adenocarcinoma; koilocytosis; hyperkeratosis; intraepithelial neoplasia;

KW intraepithelial lesion; dysplasia; head cancer; neck cancer;
 KW small cell lung cancer; melanoma; oncogene.

OS Human papillomavirus 16.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 3

FT /label= OTHER

FT /note= "OTHER- L-carboxymethylcysteine"

FT Modified-site 17

FT /label= OTHER

FT /note= "OTHER- L-carboxymethylcysteine"

PN WO20017142-A1.

PD 18-OCT-2001.

PF 05-APR-2001; 2001WO-US11233.

PR 05-APR-2000; 2000US-194796P.

PA (IMPA-) IMPACT DIAGNOSTICS INC.

PI Hu YX;

DR WPI; 2002-010888/01.

PT New peptides derived from E2, E6 or E7 early coding regions of human
 PT papillomavirus 16 and 18, useful in diagnosis of human papillomavirus
 PT infection and associated malignancy e.g. cervical carcinoma

PS Disclosure: Page 25; 28pp; English.

XX The invention describes a novel peptide derived from the E2, E6 or E7
 CC early coding region of human papillomavirus (HPV) 16 and 18, which is
 CC soluble in aqueous solution and has a lysine or cysteine residue near the
 CC amino terminus, very few tryptophan, methionine and cysteine residues,
 CC and/or many glycine and asparagine residues. The peptides and diagnostic
 CC method are used to diagnose HPV infection, especially infection with
 CC oncogenic HPV by using peptides derived from the E2 region, since HPV 16
 CC and 18 are the main HPV genetic types associated with cancers, and
 CC presence of antibodies to E2 protein is known to provide evidence of HPV
 CC infection. They are also useful to diagnose HPV associated malignancy or
 CC premalignancy, especially carcinoma by using peptides derived from the E6
 CC or E7 regions, since E6 and E7 are thought to be tumour-specific
 CC antigens. The peptides and diagnostic method are especially useful to
 CC diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix)
 CC and any HPV associated epithelial cell abnormality including high grade
 CC dysplasias, koilocytosis, hyperkeratosis, precancerous conditions
 CC encompassing intraepithelial neoplasias or intraepithelial lesions, and
 CC invasive or malignant cancers. They are also used to detect head and neck
 CC cancers, small cell lung cancers, penial and anal squamous cell carcinomas
 CC and melanoma. This is the amino acid sequence of peptide epitope #3, a
 CC synthetic peptide derived from the E2 early coding region of HPV 16, an
 CC oncoprotein involved in the integration of the viral genome into the host
 CC cell genome by the HPV types associated with malignant cancers, described


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DE Human papillomavirus protein HPV33 E2.
XX
XX Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW HPV; epitope; T cell; identification; vaccine; infection; genital wart;
KW neoplastic growth; antiviral.
XX
XX Human papillomavirus.
OS
XX WO200141799-A1.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US33549.
XX
XX 10-DEC-1999; 99US-0172705.
XX
XX 15-AUG-2000; 2000US-0641528.
XX
XX (EPTM-) EPTMONE INC.
XX
XX Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
XX
XX WPI: 2001-381497/40.
XX
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
XX treating HPV infections -
XX
XX Disclosure; Page 26; 756pp; English.
XX
XX The present invention describes an isolated prepared human papillomavirus
XX (HPV) epitope (I). (I) has antiviral activity, and can be used in
XX vaccine production. Peptides and corresponding nucleic acid compositions
XX from the present invention are useful for stimulating an immune response
XX to HPV by stimulating the production of CTL or HTL responses,
XX specifically in the treatment or prophylaxis of HPV infection, in persons
XX who have not manifested symptoms e.g. genital warts or neoplastic growth.
XX The peptides can also be used in a tetramer staining assay to assess
XX peripheral blood mononuclear cells for the presence of antigen-specific
XX CTLs following exposure to a pathogen or immunogen, and as reagents to
XX evaluate immune recall responses or evaluate the efficacy of a vaccine.
XX The vaccine compositions are useful for removing warts or treating HPV
XX infections. The epitopes for inclusion in an epitope-base vaccine may
XX be selected from conserved regions of viral or tumour-associated
XX antigens, which reduces the likelihood of escape mutants, also
XX CC immunosuppressive epitopes that may be present in whole antigens can be
XX avoided with the use of epitope-base vaccines. An additional advantage
XX CC is the ability to combine selected epitopes (CTL and HTL) and to modify
XX CC the composition of the epitopes achieving enhanced immunogenicity, the
XX major benefit of the vaccine is that is safe and efficacious. AAB98391
XX to AAB98477 represent polypeptide sequences used in the exemplification
XX of the present invention.
XX
XX Sequence 353 AA:
SQ

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Query Match 55.5%; Score 66; DB 22; Length 353;
Best Local Similarity 75.0%; Pred. No. 0.12;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 4 NPMHYNTWTHIYCEE 19
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DB 127 NTMDYTMGSEIYITEE 142

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Search completed: January 14, 2003, 18:39:54
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